

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:58 ; Search time 23.6 Seconds
(without alignments)
98.410 Million cell updates/sec

Title: US-09-989-621-1
Perfect score: 45
Sequence: 1 HSLRGLFV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacterioplasmid:*
17: sp_archaeplastid:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	82.2	154	12 Q67887	Q67887 hepatitis b
2	37	82.2	453	10 Q9LU91	Q9LU91 arabisidopsis
3	37	82.2	453	10 Q8L720	Q8L720 arabisidopsis
4	37	82.2	484	16 Q8XLS1	Q8XLS1 clostridium
5	26	80.0	1582	16 Q8XV66	Q8XV66 raistonia s
6	36	80.0	1615	16 Q8RXX2	Q8RXX2 deinococcus
7	35	77.8	66	12 Q67873	Q67873 hepatitis b
8	35	77.8	70	12 Q9YVP9	Q9YVP9 hepatitis b
9	35	77.8	70	12 Q9W8F3	Q9W8F3 hepatitis b
10	35	77.8	70	12 Q9YJA9	Q9YJA9 hepatitis b
11	35	77.8	70	12 Q9YJW2	Q9YJW2 hepatitis b
12	35	77.8	70	12 Q9WKC7	Q9WKC7 hepatitis b
13	35	77.8	70	12 Q9WKC6	Q9WKC6 hepatitis b
14	35	77.8	95	10 Q9PER0	Q9PER0 zea mays (m
15	35	77.8	97	12 Q9WP57	Q9WP57 hepatitis b
16	35	77.8	100	12 Q9WP61	Q9WP61 hepatitis b

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17 35 77.8 103 12 Q9WP79 hepatitis b
18 35 77.8 103 12 Q9JH71 hepatitis b
19 35 77.8 103 12 Q9WP49 hepatitis b
20 35 77.8 129 12 Q8QVU1 hepatitis b
21 35 77.8 129 12 Q8QVU0 hepatitis b
22 35 77.8 129 12 Q8QVT5 hepatitis b
23 35 77.8 129 12 Q8QVS7 hepatitis b
24 35 77.8 129 12 Q8QVS0 hepatitis b
25 35 77.8 129 12 Q8QVT1 hepatitis b
26 35 77.8 129 12 Q8QVU8 hepatitis b
27 35 77.8 129 12 Q8QVU7 hepatitis b
28 35 77.8 129 12 Q8QVU2 hepatitis b
29 35 77.8 129 12 Q8QVU5 hepatitis b
30 35 77.8 129 12 Q8QVT3 hepatitis b
31 35 77.8 129 12 Q8QVT0 hepatitis b
32 35 77.8 129 12 Q8QVU3 hepatitis b
33 35 77.8 129 12 Q8QVS4 hepatitis b
34 35 77.8 129 12 Q8QVT4 hepatitis b
35 35 77.8 129 12 Q8QVR9 hepatitis b
36 35 77.8 129 12 Q8QVS9 hepatitis b
37 35 77.8 129 12 Q8QVT7 hepatitis b
38 35 77.8 129 12 Q8QVT2 hepatitis b
39 35 77.8 129 12 Q8QVS3 hepatitis b
40 35 77.8 129 12 Q8QVS8 hepatitis b
41 35 77.8 129 12 Q8QVU4 hepatitis b
42 35 77.8 129 12 Q8QVS6 hepatitis b
43 35 77.8 129 12 Q8QVU6 hepatitis b
44 35 77.8 129 12 Q8QVT6 hepatitis b
45 35 77.8 129 12 Q8QVT9 hepatitis b

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ALIGNMENTS

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RESULT 1
Q67887 ID Q67887 PRELIMINARY; PRT; 154 AA.
AC Q67887;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE X protein.
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_taxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Lai M.E., Mazzoleni A.P., Melis A., Balestrieri A.;
RT "Sequence analysis of HBV genomes isolated from patients with HBsAg
RL negative chronic liver disease.";
DR EMBL; X68292; CAA48352.1; -
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16614 MW; 15F02AB57C8D7681 CRC64;

Query Match 82.2%; Score 37; DB 12; Length 154;
Best Local Similarity 88.9%; Pred. No. 6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSLRGLFV 9
Db 52 HSLRGLTV 60

RESULT 2
Q9LU91 ID Q9LU91 PRELIMINARY; PRT; 453 AA.
AC Q9LU91;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

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SEQ	SEQUENCE	453 AA;	50544 MW;	CCD32A171A903364	CR664;
Query Match	82.2%;	Score 37;	DB 10;	Length 453;	
Best Local Similarity	87.5%;	Pred. No. 18;			
Matches	7;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1 HLSLRGLF 8				
DB	325 HQLRGLF 332				
RESULT 4					
Q8XLS1					
ID	Q8XLS1 PRELIMINARY;	PRT;	484 AA.		
AC					
DT	01-WAR-2002 (TrEMBLrel. 20, Created)				
DT	01-WAR-2002 (TrEMBLrel. 20, Last sequence update)				
DT	01-WAR-2003 (TrEMBLrel. 23, Last annotation update)				
DE	Probable Na+/H+ antiporter.				
DE	CPE0970.				
OS	Clostridium perfringens.				
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;				
OC	Clostridium.				
OX	NCBI_TaxID=1502;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RP	STRAIN=13 / Type A;				
RC	PubMed=11792842;				
RA	Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,				
RA	Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;				
RT	"Complete genome sequence of Clostridium perfringens, an anaerobic				
RT	flesh-eater.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).				
DR	EMBL; AP003188; BAB80676.1; -;				
DR	InterPro; IPR006153; Na_H_porter.				
DR	InterPro; IPR006037; TrkAC.				
DR	Pfam; PF00999; Na_H_Exchange; 1.				
DR	Pfam; PF02080; TrkA-C; 1.				
KW	Complete proteome.				
SQ	SEQUENCE 484 AA; 53525 MW; 5C061DD5A26C0739	CR664;			
Query Match	82.2%;	Score 37;	DB 16;	Length 484;	
Best Local Similarity	77.8%;	Pred. No. 20;			
Matches	7;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1 HLSLRGLF 9				
DB	224 HSLVRGLFV 232				
RESULT 5					
Q8XV66					
ID	Q8XV66 PRELIMINARY;	PRT;	1582 AA.		
AC					
DT	01-WAR-2002 (TrEMBLrel. 20, Created)				
DT	01-WAR-2002 (TrEMBLrel. 20, Last sequence update)				
DT	01-WAR-2003 (TrEMBLrel. 23, Last annotation update)				
DE	Probable glutamate synthase (Large subunit) oxidoreductase protein				
DE	(EC 1.4.1.13).				
OS	GLTB OR RSC2965 OR RS01332.				
GN	Ralstonia solanacearum (Pseudomonas solanacearum).				
OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;				
OC	Ralstoniaceae; Ralstonia.				
OX	NCBI_TaxID=305;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RP	STRAIN=GMI1000;				
RC	MEDLINE=21681879; PubMed=11823852;				
RA	Salanoubat M., Genin S., Ariguenave F., Gouzy J., Mangerot S.,				
RA	Arist M., Billault A., Brotier P., Camus J.C., Cattolico L.,				
RA	Chandler M., Choise N., Claudel-Renard C., Cunne S., Demange N.,				
RA	Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,				
RA	Siquier P., Thebaud P., Whalen M., Wincker P., Levy M.,				

RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*.";
 RL Nature 415:497-502(2002);
 DR EMBL; AL646072; CAD16672.1; -;
 DR InterPro; IPR002489; DUF14.
 DR InterPro; IPR002932; Glu_synthase.
 DR InterPro; IPR006981; Glu_synth_NTN.
 DR InterPro; IPR006982; Glu_synth_central.
 DR Pfam; PF01645; Glu_synthase; 1.
 DR Pfam; PF04897; Glu_synth_NTN; 1.
 DR Pfam; PF04898; Glu_synth_central; 1.
 DR Pfam; PF01493; GXGXG; 1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 1582 AA; 173669 MW; 7F5C498FFB59F0E9 CRC64;

Query Match 80.0%; Score 36; DB 16; Length 1582;
 Best Local Similarity 75.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSLRGLF 8
 Db 871 HMTLRGLF 878

RESULT 6
 Q9RXX2 PRELIMINARY; PRT; 1615 AA.

ID Q9RXX2
 AC Q9RXX2
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Glutamate synthase, large subunit.
 GN DR0183.
 OS Deinococcus radiodurans.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RI;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.";
 RL Science 286:1571-1577(1999).
 DR EXBL; AE001880; AAF09770.1; -;
 DR TTGR; DR0183.
 DR InterPro; IPR002489; DUF14.
 DR InterPro; IPR002932; Glu_synthase.
 DR InterPro; IPR006981; Glu_synth_NTN.
 DR InterPro; IPR006982; Glu_synth_central.
 DR Pfam; PF01645; Glu_synthase; 1.
 DR Pfam; PF04897; Glu_synth_NTN; 1.
 DR Pfam; PF04898; Glu_synth_central; 1.
 DR Pfam; PF01493; GXGXG; 1.
 KW Complete proteome.
 SQ SEQUENCE 1615 AA; 176918 MW; FE014DB1140BFE26 CRC64;

Query Match 80.0%; Score 36; DB 16; Length 1615;
 Best Local Similarity 75.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSLRGLF 8
 Db 890 HMTLRGLF 897

RESULT 7
 Q67873 PRELIMINARY; PRT; 66 AA.

ID Q67873
 AC Q67873
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE X ORF.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lai M.E., Mazzoleni A.P., Balestrieri A., Melis A., Porru A.;
 RT "Sequence analysis of HBV genomes isolated from patients with HBsAg negative chronic liver disease.";
 RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X65257; CA446351.1; -;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 SQ SEQUENCE 66 AA; 6701 MW; 2D3923207BFF8E3C CRC64;

Query Match 77.8%; Score 35; DB 12; Length 66;
 Best Local Similarity 100.0%; Pred. No. 6.7; 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSLRGL 7
 Db 52 HSLRGL 58

RESULT 8
 Q9YFV9 PRELIMINARY; PRT; 70 AA.

ID Q9YFV9
 AC Q9YFV9
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE X protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20261764; PubMed=10799618;
 RA Greche S., Heckel J.O., Rietschel W., Hufert F.T.;
 RT "Molecular epidemiology of hepatitis B virus variants in non-human primates.";
 RL J. Virol. 74:5377-5381(2000).
 DR EMBL; AJ131555; CA410413.1; -;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 FT NON_TER 70
 SQ SEQUENCE 70 AA; 7101 MW; B788B4A9B9A5CFF3 CRC64;

Query Match 77.8%; Score 35; DB 12; Length 70;
 Best Local Similarity 100.0%; Pred. No. 7.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSLRGL 7
 Db 52 HSLRGL 58

RESULT 9
 Q9W8F3 PRELIMINARY; PRT; 70 AA.

ID Q9W8F3
 AC Q9W8F3
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE X protein (Fragment).
 OS Hepatitis B virus.

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OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Grethe S., Heckel J.O., Rietschel W., Thomssen R., Hufert F.T.;
RT "Molecular epidemiology of hepatitis B virus variants in non-human
RT primates.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131556; CAA10415.1; -.
DR EMBL; AJ131553; CAA10409.1; -.
DR EMBL; AJ131554; CAA10411.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 70
SQ SEQUENCE 70 AA; 7095 MW; B79CF0F9A3EF7B17 CRC64;

Query Match 77.8%; Score 35; DB 12; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
DB 52 HLSLRGL 58

RESULT 10
QYJ9A9 PRELIMINARY; PRT; 70 AA.
ID Q9YJ9A9
AC Q9YJ9A9
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Grethe S., Heckel J.O., Rietschel W., Thomssen R., Hufert F.T.;
RT "Molecular epidemiology of hepatitis B virus variants in non-human
RT primates.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131558; CAA10419.1; -.
DR EMBL; AJ131557; CAA10417.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 70
SQ SEQUENCE 70 AA; 7099 MW; B79CF0F9A3EF7F13 CRC64;

Query Match 77.8%; Score 35; DB 12; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
DB 52 HLSLRGL 58

RESULT 11
QYJ9W2 PRELIMINARY; PRT; 70 AA.
ID Q9YJ9W2
AC Q9YJ9W2
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE X protein (fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Grethe S., Heckel J.O., Rietschel W., Hufert F.T.;

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RT "Molecular epidemiology of hepatitis B virus variants in non-human
RT primates.";
RL J. Virol. 74:5377-5381(2000).
DR EMBL; AJ131551; CAA10405.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 70
SQ SEQUENCE 70 AA; 7064 MW; 621D545CA24BD293 CRC64;

Query Match 77.8%; Score 35; DB 12; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
DB 52 HLSLRGL 58

RESULT 12
Q9WK7 PRELIMINARY; PRT; 70 AA.
ID Q9WK7
AC Q9WK7
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE X protein (fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Grethe S., Heckel J.O., Rietschel W., Hufert F.T.;
RT "Molecular epidemiology of hepatitis B virus variants in non-human
RT primates.";
RL J. Virol. 74:5377-5381(2000).
DR EMBL; AJ131548; CAA10399.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 70
SQ SEQUENCE 70 AA; 7100 MW; A5114820ECF8DE17 CRC64;

Query Match 77.8%; Score 35; DB 12; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
DB 52 HLSLRGL 58

RESULT 13
Q9WK6 PRELIMINARY; PRT; 70 AA.
ID Q9WK6
AC Q9WK6
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE X protein (fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Grethe S., Heckel J.O., Rietschel W., Hufert F.T.;
RT "Molecular epidemiology of hepatitis B virus variants in non-human
RT primates.";
RL J. Virol. 74:5377-5381(2000).
DR EMBL; AJ131550; CAA10403.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 70

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SQ SEQUENCE 70 AA; 7128 MW; B99B88D20CB9CC0C CRC64;

Query Match 77.8%; Score 35; DB 12; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.1; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HLSLRGL 7
Db 52 HLSLRGL 58

RESULT 14

Q9PERO

ID Q9PERO PRELIMINARY; PRT; 95 AA.

AC Q9PERO;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Basal layer antifungal peptide precursor.
GN BAP-3B.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1] _
RP SEQUENCE FROM N.A.
RC TISSUE=Endosperm;
RA Serna Sanz A., Thompson R.D.;
RT "Maize endosperm secretes a novel antifungal protein into adjacent
RT maternal tissue."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AJ297903; CAC21607.1; -
KW Signal.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 95 BAP-3B PROTEIN.
SQ SEQUENCE 95 AA; 11076 MW; 82B4F67B9512D243 CRC64;

Query Match 77.8%; Score 35; DB 10; Length 95;
Best Local Similarity 55.6%; Pred. No. 9.7; Indels 0; Gaps 0;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 HLSLRGLFV 9
Db 7 HITIRGLFL 15

RESULT 15

Q9WPS7

ID Q9WPS7 PRELIMINARY; PRT; 97 AA.

AC Q9WPS7;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE X protein.
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1] _
RP SEQUENCE FROM N.A.
RX MEDLINE=20037832; PubMed=10573161;
RA Freixschat P., Meisel H., Will H., Gunther S.;
RT "Hepatitis B virus genomes from long-term immunosuppressed virus
RT carriers are modified by specific mutations in several regions."
RL J. Gen. Virol. 80:2685-2691(1999).
RN [2]

RP SEQUENCE FROM N.A.

RA Freixschat P., Meisel H., Iwanska A., Will H., Gunther S.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF143306; AAD37956.1; -
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.

SQ SEQUENCE 97 AA; 10051 MW; 47445E0D2909A897 CRC64;

Query Match 77.8%; Score 35; DB 12; Length 97;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HLSLRGL 7
Db 52 HLSLRGL 58

Search completed: December 23, 2003, 08:46:07
Job time : 27.6 secs

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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 11 seconds
(without alignments)
78.683 Million cell updates/sec

Title: US-09-989-621-1

Perfect score: 45

Sequence: 1 HLSLRGLFV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 76:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	37	82.2	154	2	S25650	gene X protein - h
2	37	82.2	1436	2	A46496	antigen WC1.1 prec
3	36	80.0	1615	2	C75551	glutamate synthase
4	35	77.8	66	2	S20747	gene X protein - h
5	35	77.8	134	1	B48345	gene X protein, tr
6	35	77.8	154	1	QQVLD1	gene X protein - h
7	35	77.8	154	1	A48345	gene X protein - h
8	35	77.8	154	1	QQVLH1	gene X protein - h
9	35	77.8	154	1	QQVLAI	gene X protein - h
10	35	77.8	154	1	QQVLAW	gene X protein - h
11	35	77.8	154	1	QQVLKS	gene X protein - h
12	35	77.8	154	1	QQVLCP	gene X protein - h
13	35	77.8	154	2	S20756	gene X protein - h
14	35	77.8	154	2	S47408	gene X protein - h
15	35	77.8	154	2	S47408	gene X protein - h
16	35	77.8	154	2	JS0256	gene X protein - h
17	35	77.8	154	2	S67503	gene X protein - h
18	35	77.8	154	2	JS0228	trans-activating p
19	35	77.8	154	2	S53130	gene X protein - h
20	35	77.8	154	2	JS0603	gene X protein - h
21	35	77.8	154	2	JS0604	gene X protein - h
22	35	77.8	154	2	S35529	gene X protein - h
23	35	77.8	154	2	S33687	gene X protein - h
24	35	77.8	154	2	S12542	gene X protein - h
25	35	77.8	154	2	S32203	gene X protein - h
26	35	77.8	154	2	S23219	gene X protein - h
27	35	77.8	154	2	S20751	gene X protein - h
28	35	77.8	154	2	T13466	gene X protein - h
29	35	77.8	172	2	A58456	X protein - human

30 35 77.8 210 2 T13472 gene X protein - h
31 35 77.8 210 2 S12598 gene X protein - h
32 35 77.8 359 2 S04570 gene X/C fusion pr
33 35 77.8 451 2 G83916 glycolate oxidase
34 34 75.6 178 2 S29119 hypothetical prote
35 34 75.6 361 2 S30325 hypothetical prote
36 34 75.6 1200 2 C96025 hypothetical expor
37 33 73.3 195 2 JC2258 substate protein
38 33 73.3 569 2 AB0005 probable exported
39 32 71.1 296 2 B83417 hypothetical prote
40 32 71.1 368 2 C81284 cystathionine beta
41 32 71.1 369 2 B75511 dihydroorotate deh
42 32 71.1 430 2 H91259 hypothetical prote
43 32 71.1 430 2 D86100 hypothetical prote
44 32 71.1 430 2 A65215 hypothetical 49.4
45 32 71.1 509 2 B86667 alkyl hydroperoxid

ALIGNMENTS

RESULT 1

S25650
gene X protein - hepatitis B virus (subtype ayw, patient D)
C:Species: hepatitis B virus, HBV
A:Variety: subtype ayw, patient D
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S25650
R:Lai, M.E.; Mazzoleni, A.P.; Mellis, A.; Balestrieri, A.
submitted to the EMBL Data Library, September 1992
A:Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negati
A:Reference number: S25650
A:Accession: S25650
A:Molecule type: DNA
A:Residues: 1-154 <LAI>
A:Cross-references: EMBL:X68292; NID:G59448; PIDD:CAA48352.1; PIDD:G59449
A:Experimental source: subtype ayw, patient D
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 82.2%; Score 37; DB 2; Length 154;
Best Local Similarity 88.9%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 HLSLRGLFV 9
Db 52 HLSLRGLTV 60

RESULT 2

A46496
antigen WC1.1 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 18-Jun-1993 #sequence_revision 19-May-1994 #text_change 05-Nov-1999
C:Accession: A46496; I45834; S19913
R:Wijngaard, P.L.; Metzelaar, M.J.; MacHugh, N.D.; Morrison, W.I.; Clevers, H.C.
J. Immunol. 149, 3273-3277, 1992
A:Title: Molecular characterization of the WC1 antigen expressed specifically on bovine
A:Reference number: A46496; MUID:93056489; PMID:1431105
A:Accession: A46496
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1436 <WJ>
A:Cross-references: EMBL:X63723; NID:g13; PIDD:CAA45255.1; PIDD:g14
A:Experimental source: CD4-CD8- gamma delta T lymphocytes
A>Note: sequence extracted from NCBI backbone (NCBIP:117475)
R:Wijngaard, P.L.; MacHugh, N.D.; Metzelaar, M.J.; Romberg, S.; Bensaid, A.; Pepin, L.;
J. Immunol. 152, 3476-3482, 1994
A:Title: Members of the novel WC1 gene family are differentially expressed on subsets of
A:Reference number: I45834; MUID:94194107; PMID:7511649
A:Accession: I45834
A>Status: preliminary; translated from GS/EMBL/DBU

A:Molecule type: mRNA
A:Residues: 1-1436 <WI2>
A:Cross-references: EMBL:X63723; NID:g13; PIDN:CAA45255.1; PID:g14
C:Genetics:
A:Gene: WC1.1
C:Superfamily: scavenger receptor cysteine-rich domain homology
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-1436/Product: WC1 antigen #status predicted <MAT>
F:125-131/Domain: scavenger receptor cysteine-rich domain homology
F:132-234/Domain: scavenger receptor cysteine-rich domain homology <SR01>
F:236-340/Domain: scavenger receptor cysteine-rich domain homology <SR02>
F:373-476/Domain: scavenger receptor cysteine-rich domain homology <SR03>
F:478-581/Domain: scavenger receptor cysteine-rich domain homology <SR04>
F:583-686/Domain: scavenger receptor cysteine-rich domain homology <SR05>
F:687-789/Domain: scavenger receptor cysteine-rich domain homology <SR06>
F:791-895/Domain: scavenger receptor cysteine-rich domain homology <SR07>
F:928-1031/Domain: scavenger receptor cysteine-rich domain homology <SR08>
F:1033-1136/Domain: scavenger receptor cysteine-rich domain homology <SR10>
F:1152-1255/Domain: scavenger receptor cysteine-rich domain homology <SR11>

Query Match 82.2%; Score 37; DB 2; Length 1436;
Best Local Similarity 88.9%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 HLSLRGLFV 9
DB 6 HLSLRGLCV 14
|||||

RESULT 3
C75551
Glutamate synthase (NADH2) (EC 1.4.1.14) large chain DR0183 precursor [similarity] - Dein
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Jun-2002
C:Accession: C75551
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: C75551
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1615 <WHI>
A:Cross-references: GB:AE001980; GB:AE000513; NID:G6457844; PIDN:AAF09770.1; PID:G645783
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0183
A:Map position: 1
C:Superfamily: glutamate synthase (NADPH)
C:Keywords: 3Fe-4S; metalloprotein; oxidoreductase
F:1-52/Domain: propeptide #status predicted <PRO>
F:53-1615/Product: glutamate synthase #status predicted <MAT>
F:53/Active site: Cys #status predicted
F:1198,1204,1209/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 80.0%; Score 36; DB 2; Length 1615;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY -1 HLSLRGLF 8
DB 890 HMTLRGLF 897
|||||

RESULT 4
S20747
gene x protein - hepatitis B virus (subtype ayw, patient C)
C:Species: hepatitis B virus, HBV
A:Variety: subtype ayw, patient C
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S20747

R:Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Melis, A.; Porru, A.
submitted to the EMBL Data Library, March 1992
A:Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negat
A:Reference number: S20745
A:Accession: S20747
A:Molecule type: DNA
A:Residues: 1-66 <LAI>
A:Cross-references: EMBL:X65257; NID:G59429; PIDN:CAA46351.1; PID:G59432
A:Experimental source: subtype ayw, patient C
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HLSLRGL 7
DB 52 HLSLRGL 58
|||||

RESULT 5
B48345
gene x protein, truncated form - hepatitis B virus
C:Species: hepatitis B virus, HBV
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C:Accession: B48345
R:Repp, R.; Keller, C.; Borkhardt, A.; Csecke, A.; Schaefer, S.; Gerlich, W.H.; Lampert
Arch. Virol. 125, 299-304, 1992
A:Title: Detection of a hepatitis B virus variant with a truncated X gene and enhancer
A:Reference number: A48345; MUID:92352333; PMID:1642555
A:Accession: B48345
A:Molecule type: DNA
A:Residues: 1-134 <REP>
A:Cross-references: GB:IS41176; NID:G252541; PIDN:AAB22733.1; PID:G252542
A:Note: sequence extracted from NCBI backbone (NCBI:109914, NCBI:P:109915)
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HLSLRGL 7
DB 52 HLSLRGL 58
|||||

RESULT 6
QOVLDI
gene x protein - hepatitis B virus (subtype ayw)
C:Species: hepatitis B virus, HBV
C:Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 08-Apr-1994
C:Accession: A03719
R:Galibert, F.; Mandart, E.; Fitoussi, F.; Tiollais, P.; Charnay, P.
Nature 281, 646-650, 1979
A:Title: Nucleotide sequence of the hepatitis B virus genome (subtype ayw) in E. coli.
A:Reference number: A93214; MUID:81013091; PMID:399327
A:Accession: A03719
A:Molecule type: DNA
A:Residues: 1-154 <GAL>
A:Cross-references: GB:J02203; GB:V01460
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HLSLRGL 7

Db 52 HLSLRGL 58
|||||

RESULT 7

QOVLBH
Gene X protein - hepatitis B virus (subtype ayw, strain PHB320)
C:Species: hepatitis B virus, HBV
A:Variety: subtype ayw, strain PHB320
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: A05237; S53144; S53173; S53195; S53210; S53217; S53222; S53224; S53235; S53280
R:Bickho, V.; Pushko, P.; Dreilina, D.; Pumpen, P.; Gren, E.
FEBS Lett. 185, 208-212, 1985
A:Title: Subtype ayw variant of hepatitis B virus: DNA primary structure analysis.
A:Reference number: A05237; MUID:85204397; PMID:3996597
A:Accession: A05237
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-154 <BIC>
A:Cross-references: EMBL:X02496; NID:962280; PIDN:CAB41697.1; PID:G4704317
A:Experimental source: subtype ayw, strain PHB320
R:Lai, M.B.; Mazoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A:Reference number: S53112
A:Accession: S53144
A:Molecule type: DNA
A:Residues: 124-154 <LA1>
A:Cross-references: EMBL:X85267; NID:G736025; PIDN:CAA59548.1; PID:G736026; EMBL:X85284; S5305; EMBL:X85307; EMBL:X85308; EMBL:X85310; EMBL:X85312; EMBL:X85315; EMBL:X85316
A:Experimental source: isolate patient Pintus'85 et al.
A:Accession: S53173
A:Molecule type: DNA
A:Residues: 124-154 <LA2>
A:Cross-references: EMBL:X85277; NID:G736065; PIDN:CAA59575.1; PID:G736066
A:Experimental source: isolate patient Bio'90
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSLRGL 7
|||||

Db 52 HSLRGL 58

RESULT 8

A48345
Gene X protein - hepatitis B virus
C:Species: hepatitis B virus, HBV
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C:Accession: A48345
R:Repp, R.; Keller, C.; Borkhardt, A.; Csecke, A.; Schaefer, S.; Gerlich, W.H.; Lampert, Arch. Virol. 125, 299-304, 1992
A:Title: Detection of a hepatitis B virus variant with a truncated X gene and enhancer I
A:Reference number: A48345; MUID:92352333; PMID:1642555
A:Accession: A48345
A:Molecule type: DNA
A:Residues: 1-154 <REP>
A:Cross-references: GB:S41175; NID:G252539; PIDN:AAB22732.1; PID:G252540
A:Note: sequence extracted from NCBI backbone (NCBIN:109912, NCBI:P:109913)
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSLRGL 7
|||||

Db 52 HSLRGL 58
|||||

RESULT 9

QOVLAI
Gene X protein - hepatitis B virus (strain alpha1)
C:Species: hepatitis B virus, HBV
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: D34773
R:Tong, S.; Li, J.; Vitvitski, L.; Trepo, C.
Virology 176, 596-603, 1990
A:Title: Active hepatitis B virus replication in the presence of anti-HBe is associated
A:Reference number: A34773; MUID:90266476; PMID:2345966
A:Accession: D34773
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-154 <TON>
A:Cross-references: EMBL:M32138; NID:G329667; PIDN:AAA45504.1; PID:G329671
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSLRGL 7
|||||

Db 52 HSLRGL 58

RESULT 10

QOVLAW
Gene X protein - hepatitis B virus (subtype adw and adw2)
C:Species: hepatitis B virus, HBV
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 30-Jun-1998
C:Accession: A31289; B94409; A03719
R:Lo, S.J.; Chien, M.L.; Lee, Y.H.W.
Virology 167, 289-292, 1988
A:Title: Characteristics of the X gene of hepatitis B virus.
A:Reference number: A31289; MUID:89045656; PMID:3188399
A:Accession: A31289
A:Molecule type: DNA
A:Residues: 1-154 <LOS>
A:Experimental source: subtype adw
R:Valenzuela, P.; Quiroga, M.; Zaldivar, J.; Gray, P.; Rutter, W.J.
in Animal Virus Genetics, Field, B.N., Jaenisch, R., and Fox, C.F., eds., pp.57-70, Acad

Query Match 77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSLRGL 7
|||||

Db 52 HSLRGL 58

RESULT 11

QOVLKS
Gene X protein - hepatitis B virus (subtype adw, strain 991)
C:Species: hepatitis B virus, HBV
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: S10380
R:Koechel, H.G.; Schueler, A.; Lottmann, S.; Thomsen, R.
Query Match 77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSLRGL 7
|||||

Db 52 HSLRGL 58

submitted to the EMBL Data Library, February 1990

A:Reference number: S10380
A:Accession: S10380
A:Molecule type: DNA
A:Residues: 1-154 <KOE>
A:Cross-references: EMBL:X51970; NID:g1155012; PIDN:CAA36231.1; PID:g60432
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred.No. 8.7; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 HLSLRL 7
Db 52 HLSLRL 58

RESULT 12

COVLCPC
gene X protein - hepatitis B virus (strain LSH, chimpanzee)
C:Species: hepatitis B virus, HBV
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jun-2000
C:Accession: D28885
R:Vaudin, M.; Wolstenholme, A.J.; Tsiuaye, K.N.; Zuckerman, A.J.; Harrison, T.J.
J. Gen. Virol. 69, 1383-1389, 1988
A:Title: The complete nucleotide sequence of the genome of a hepatitis B virus isolated
A:Reference number: A92796; MUID:86258473; PMID:2838576
A:Accession: D28885
A:Molecule type: DNA
A:Residues: 1-154 <VAU>
A:Cross-references: GB:D00220; NID:g221505; PIDN:BAA00160.1; PID:g221509
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred.No. 8.7; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 HLSLRL 7
Db 52 HLSLRL 58

RESULT 13

S20756
gene X protein - hepatitis B virus (subtype ayw, patient E)
C:Species: hepatitis B virus, HBV
A:Variety: subtype ayw, patient E
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S20756
R:Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Mellis, A.; Porru, A.
submitted to the EMBL Data Library March 1992
A:Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negative
A:Reference number: S20745
A:Accession: S20756
A:Molecule type: DNA
A:Residues: 1-154 <LAI>
A:Cross-references: EMBL:X65259; NID:g59439; PIDN:CAA46360.1; PID:g59443
A:Experimental source: subtype ayw, patient E
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 2; Length 154;
Best Local Similarity 100.0%; Pred.No. 8.7; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 HLSLRL 7
Db 52 HLSLRL 58

RESULT 14

S47404
gene X protein - hepatitis B virus (subtype ayw4)
C:Species: hepatitis B virus, HBV
A:Variety: subtype ayw4
C:Date: 23-Nov-1994 #sequence_revision 12-May-1995 #text_change 26-Aug-1999
C:Accession: S47404
R:Plucienniczak, A.
submitted to the EMBL Data Library, August 1994
A:Description: Molecular cloning and sequencing of two complete genomes of polish isola
A:Reference number: S47404
A:Accession: S47404
A:Molecule type: DNA
A:Residues: 1-154 <PLU>
A:Cross-references: EMBL:Z35716; NID:g527435; PIDN:CAA84785.1; PID:g527436
A:Experimental source: subtype ayw4
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 2; Length 154;
Best Local Similarity 100.0%; Pred.No. 8.7; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 HLSLRL 7
Db 52 HLSLRL 58

RESULT 15

S47408
gene X protein - hepatitis B virus (subtype adw2)
C:Species: hepatitis B virus, HBV
A:Variety: subtype adw2
C:Date: 23-Nov-1994 #sequence_revision 12-May-1995 #text_change 26-Aug-1999
C:Accession: S47408
R:Plucienniczak, A.
submitted to the EMBL Data Library, August 1994
A:Description: Molecular cloning and sequencing of two complete genomes of polish isola
A:Reference number: S47408
A:Accession: S47408
A:Molecule type: DNA
A:Residues: 1-154 <PLU>
A:Cross-references: EMBL:Z35717; NID:g527440; PIDN:CAA84789.1; PID:g527441
A:Experimental source: subtype adw2
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 2; Length 154;
Best Local Similarity 100.0%; Pred.No. 8.7; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 HLSLRL 7
Db 52 HLSLRL 58

Search completed: December 23, 2003, 08:41:04
Job time : 14 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 25.8 Seconds
(without alignments)
55.370 Million cell updates/sec

Title: US-09-989-621-1

Perfect score: 45

Sequence: 1 HSLRGLFV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	9	20	AA1980.DAT.*
2	37	82.2	1436	20	AA1981.DAT.*
3	35	77.8	8	23	AA1982.DAT.*
4	35	77.8	9	15	AA1983.DAT.*
5	35	77.8	9	23	AA1984.DAT.*
6	35	77.8	9	23	AA1985.DAT.*
7	35	77.8	9	23	AA1986.DAT.*
8	35	77.8	9	23	AA1987.DAT.*
9	35	77.8	9	23	AA1988.DAT.*

10	35	77.8	9	23	AA1989.DAT.*
11	35	77.8	9	23	AA1990.DAT.*
12	35	77.8	10	23	AA1991.DAT.*
13	35	77.8	11	23	AA1992.DAT.*
14	35	77.8	11	23	AA1993.DAT.*
15	35	77.8	11	23	AA1994.DAT.*
16	35	77.8	11	23	AA1995.DAT.*
17	35	77.8	11	23	AA1996.DAT.*
18	35	77.8	11	23	AA1997.DAT.*
19	35	77.8	11	23	AA1998.DAT.*
20	35	77.8	15	19	AA1999.DAT.*
21	35	77.8	15	19	AA2000.DAT.*
22	35	77.8	15	23	AA2001.DAT.*
23	35	77.8	15	23	AA2002.DAT.*
24	35	77.8	15	23	AA2003.DAT.*
25	35	77.8	15	23	AA2004.DAT.*
26	35	77.8	15	23	AA2005.DAT.*
27	35	77.8	15	23	AA2006.DAT.*
28	35	77.8	134	16	AA2007.DAT.*
29	35	77.8	146	22	AA2008.DAT.*
30	35	77.8	153	22	AA2009.DAT.*
31	35	77.8	154	6	AA2010.DAT.*
32	35	77.8	154	9	AA2011.DAT.*
33	35	77.8	154	21	AA2012.DAT.*
34	35	77.8	154	21	AA2013.DAT.*
35	35	77.8	154	21	AA2014.DAT.*
36	34	75.6	25	23	AA2015.DAT.*
37	34	75.6	124	22	AA2016.DAT.*
38	33	73.3	50	22	AA2017.DAT.*
39	33	73.3	144	22	AA2018.DAT.*
40	33	73.3	200	22	AA2019.DAT.*
41	33	73.3	224	21	AA2020.DAT.*
42	33	73.3	256	22	AA2021.DAT.*
43	33	73.3	256	23	AA2022.DAT.*
44	33	73.3	510	23	AA2023.DAT.*
45	33	73.3	526	21	AA2024.DAT.*

ALIGNMENTS

RESULT 1

AA1980.DAT.*

ID AA1980.DAT.* standard; peptide; 9 AA.

AC AA1980.DAT.*

DT 23-SEP-1999 (first entry)

DE Hepatitis B virus X protein peptide #1.

KW Hepatitis B virus; HBV; X protein; cytotoxic T lymphocyte; liposome;

KW CTL; antigen; immunity; liver cancer.

OS Hepatitis B virus.

OS Synthetic.

PN WO9936434-A1.

DD 22-JUL-1999.

PF 19-JAN-1998; 98WO-KR00010.

PR 19-JAN-1998; 98WO-KR00010.

XX (MOGA-) MOGAM BIOTECHNOLOGY RES INST.

XX Chang J, Cheong H, Cho S, Choi M, Hwang Y, Kim T;

XX Lee K;

XX WPI, 1999-444387/37.

XX Hepatitis B virus protein X-derived peptide antigens used to

Handwritten signature

PT stimulate cytotoxic T lymphocytes, useful for treatment of
 PT HBV-associated diseases, especially liver cancer
 XX
 PS Claim 1; Page 24; 33pp; English.
 CC The present invention describes peptide antigens AAY24459 to AAY24463
 CC derived from the X protein of hepatitis B virus (HBV) which are
 CC recognized by cytotoxic T lymphocytes (CTL). The peptide antigens
 CC derived from HBV X protein are useful for inducing CTLs against the
 CC virus or inducing immunological tolerance to the virus. pH-sensitive
 CC liposomes containing the peptide antigens are used to induce cellular
 CC immunity so that CTLs specific to the virus can be produced. This is
 CC useful for prevention and treatment of HBV-associated diseases,
 CC especially HBV-associated liver cancer. pH-sensitive liposomes permit
 CC the selective transportation of anti-cancer drugs.
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 45; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HLSLRGLFV 9
 DB 1 HLSLRGLFV 9
 RESULT 2
 AAB66088
 ID AAB66088 standard; Protein; 1436 AA.
 XX
 AC AAB66088;
 DT 30-MAR-2001 (first entry)
 DE Bovine WC1 protein.
 XX
 KW Gene therapy; TANGO protein; INTERCEPT protein; neurological disorder;
 KW central nervous system; focal brain disorder; bipolar affective disorder;
 KW global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease;
 KW senile dementia; Huntington's disease; amyotrophic lateral sclerosis;
 KW Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep;
 KW neuropsychiatric; psychoactive substance use; anxiety.
 XX
 OS Bos sp.
 PN WO200077239-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 24-MAY-2000; 2000WO-US14858.
 XX
 PR 14-JUN-1999; 99US-0333159.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI McCarthy SA, Fraser CC, Sharp JD, Barnes TW;
 XX
 DR WPI; 2001-032313/04.
 XX
 DR N-PSDB; AAF45141.
 XX
 PT TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for
 PT screening assays and diagnostic assays and for the treatment of
 PT neurological diseases such as Alzheimer's, Parkinson's and Huntington's
 PT disease -
 XX
 PS Disclosure; Fig 2; 359pp; English.
 XX
 CC The present invention relates to TANGO or INTERCEPT proteins and coding
 CC sequences (see AAF45121-F45136 and AAF45138-F45139 and AAB66031-B66057,
 CC AAB66064-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding
 CC sequences are useful for the treatment of neurological disorders such as
 CC central nervous system (CNS) disorders, CNS-related disorders, focal

CC brain disorders, global-diffuse cerebral disorders and other
 CC neurological and cerebrovascular disorders. The CNS disorders include
 CC Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic
 CC lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome,
 CC autonomic function disorders such as hypertension and sleep disorders,
 CC neuropsychiatric disorders, psychoactive substance use disorders,
 CC anxiety, and bipolar affective disorder. The present sequence is a
 CC sequence used in a sequence homology alignment with the TANGO/INTERCEPT
 CC sequences of the present invention.
 XX
 SQ Sequence 1436 AA;
 Query Match 82.2%; Score 37; DB 22; Length 1436;
 Best Local Similarity 88.9%; Pred. No. 72;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLSLRGLFV 9

DB 6 HLSLRGLCV 14

RESULT 3

ID ABJ07014 standard; Peptide; 8 AA.
 XX
 AC ABJ07014;
 XX
 DT 14-NOV-2002 (first entry)
 XX
 DE Hepatitis B virus epitope #1232.
 XX
 KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 KW virucide; hepatotropic; antiinflammatory.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200219986-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 08-SEP-2000; 2000WO-US24802.
 XX
 PR 08-SEP-2000; 2000WO-US24802.
 XX
 PA (EPIM-) EPIMUNE INC.
 PA (SETT/) SETTE A.
 XX
 PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 PI Celis E, Kubo RT, Grey HM, Chesnut RW;
 XX
 DR WPI; 2002-643192/59.
 XX
 PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
 PT infection, and/or for stimulating an immune response to HBV, comprises
 PT a HBV peptide epitope -
 XX
 PS Disclosure; Page 134; 228pp; English.
 XX
 CC The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention.
 XX
 SQ Sequence 8 AA;

Query Match 77.8%; Score 35; DB 23; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7

DB 2 HLSLRGL 8

```

RESULT 4
AAR59205
ID AAR59205 standard; peptide; 9 AA.
XX
AC AAR59205;
XX
XX
DT 25-MAR-2003 (updated)
DT 03-MAY-1995 (first entry)
XX
XX
DE Peptide fragment (1.0212) of HBV binds HLA-A2.1.
XX
XX
KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVc; EBV;
KW HIV1; core antigen; surface antigen; pharmaceutical composition;
KW in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule;
KW major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor;
KW human leukocyte antigen.
XX
XX
OS Hepatitis B Virus adr.
XX
PN WO9420127-A1.
XX
PD 15-SEP-1994.
XX
PF 04-MAR-1994; 94WO-US02353.
XX
PR 05-MAR-1993; 93US-0027146.
PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
XX
PA (CYTE-) CYTEL CORP.
XX
PI Grey HM, Kast WM, Sette A, Sidney J;
XX
DR WPI; 1994-302678/37.
XX
PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
PT for treatment or prophylaxis of cancer, virus infection or
PT autoimmune diseases.
XX
PS Example 5; Page 104; 138pp; English.
XX
XX
CC AAR59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1
CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity
CC of at least 1% as compared to a reference peptide (AAR71293). AAR59205
CC has an IC50 of 0.0004 and the sequence occurs at position 1470 in the HBV
CC "X" protein (as given in the specification). The peptides of the
CC invention can induce cytotoxic T lymphocytes which can react with target
CC cells. They can be used for the treatment or prophylaxis of cancer, eg.
CC prostate cancer or lymphoma, etc.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 9 AA;
XX
Query Match 77.8%; Score 35; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
Db 1 HLSLRGL 7

RESULT 6
ABJ06063
ID ABJ06063 standard; Peptide; 9 AA.
XX
AC ABJ06063;
XX
DT 14-NOV-2002 (first entry)
XX
DE Hepatitis B virus epitope #281.
XX
KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
KW virucide; hepatotropic; antiinflammatory.
XX
XX
OS Hepatitis B virus.
XX
PN WO200219986-A1.
XX
PD 14-MAR-2002.
XX
PF 08-SEP-2000; 2000WO-US24802.
XX
PR 08-SEP-2000; 2000WO-US24802.
XX
PA (EPIM-) EPIMMUNE INC.
PA (SETT/) SETTE A.
XX
XX
PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
PI Celis E, Kubo RT, Grey HM, Chesnut RW;
XX
DR WPI; 2002-643192/69.
XX

```

XX HBV; X protein; cytotoxic T-lymphocyte; CTL; MHC class I;
 XX major histocompatibility complex; immunomodulator.
 OS Hepatitis B virus.
 XX
 XX KR98022440-A.
 XX
 PD 06-JUL-1998.
 XX
 PF 23-SEP-1996; 96KR-0041612.
 XX
 PR 23-SEP-1996; 96KR-0041612.
 XX
 XX (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
 XX
 PI Park SH, Chung MG, Lee HG, Yoon HS, Min SS, Lee TG, Lim JS;
 XX
 XX WPI; 1999-300977/25.
 XX
 XX Synthetic peptide having immunoregulating activities for hepatitis B
 PT virus -
 XX
 XX Example 1; Page 4; 7pp; Korean.
 XX
 CC The invention relates to peptides derived from the hepatitis B virus
 CC (HBV) X protein (AAM52970-AAM52973). The peptides are presented on major
 CC histocompatibility complex (MHC) class I molecules and act as cytotoxic
 CC T-lymphocyte (CTL) epitopes. Sequences AAM52974-AAM52984 represent HBV
 CC X protein-derived peptides used in an exemplification of the invention.
 XX
 SQ Sequence 9 AA;
 XX
 Query Match 77.8%; Score 35; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
 Db 1 HLSLRGL 7

RESULT 6
 ABJ06063
 ID ABJ06063 standard; Peptide; 9 AA.
 XX
 AC ABJ06063;
 XX
 DT 14-NOV-2002 (first entry)
 XX
 DE Hepatitis B virus epitope #281.
 XX
 KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 KW virucide; hepatotropic; antiinflammatory.
 XX
 XX
 OS Hepatitis B virus.
 XX
 PN WO200219986-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 08-SEP-2000; 2000WO-US24802.
 XX
 PR 08-SEP-2000; 2000WO-US24802.
 XX
 PA (EPIM-) EPIMMUNE INC.
 PA (SETT/) SETTE A.
 XX
 XX
 PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 PI Celis E, Kubo RT, Grey HM, Chesnut RW;
 XX
 DR WPI; 2002-643192/69.
 XX

PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
 PT infection, and/or for stimulating an immune response to HBV, comprises
 PT a HBV peptide epitope -

PS Disclosure; Page 115; 228pp; English.

CC The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention.

SQ Sequence 9 AA;

Query Match 77.8%; Score 35; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
 |||||
 Db 3 HLSLRGL 9

RESULT 7
 ABJ06091
 ID ABJ06091 standard; Peptide; 9 AA.

XX AC ABJ06091;

XX DT 14-NOV-2002 (first entry)

XX DE Hepatitis B virus epitope #309.

XX KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 XX virucide; hepatotropic; antiinflammatory.

XX OS Hepatitis B virus.

XX PN WO200219986-A1.

XX PD 14-MAR-2002.

XX PF 08-SEP-2000; 2000WO-US24802.

XX PR 08-SEP-2000; 2000WO-US24802.

XX PA (EPIM-) EPIMUNE INC.

XX PA (SETT/) SETTE A.

XX PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 XX Celis E, Kubo RT, Grey HM, Chesnut RW;

XX DR WPI; 2002-643192/69.

XX PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
 PT infection, and/or for stimulating an immune response to HBV, comprises
 PT a HBV peptide epitope -

PS Disclosure; Page 115; 228pp; English.

CC The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention.

SQ Sequence 9 AA;

Query Match 77.8%; Score 35; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7

Db 1 HLSLRGL 7
 |||||

RESULT 8

ABJ07228
 ID ABJ07228 standard; Peptide; 9 AA.

XX AC ABJ07228;

XX DT 14-NOV-2002 (first entry)

XX DE Hepatitis B virus epitope #1446.

XX KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 XX virucide; hepatotropic; antiinflammatory.

XX OS Hepatitis B virus.

XX PN WO200219986-A1.

XX PD 14-MAR-2002.

XX PF 08-SEP-2000; 2000WO-US24802.

XX PR 08-SEP-2000; 2000WO-US24802.

XX PA (EPIM-) EPIMUNE INC.

XX PA (SETT/) SETTE A.

XX PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 XX Celis E, Kubo RT, Grey HM, Chesnut RW;

XX DR WPI; 2002-643192/69.

XX PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
 PT infection, and/or for stimulating an immune response to HBV, comprises
 PT a HBV peptide epitope -

PS Disclosure; Page 138; 228pp; English.

XX The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention.

XX SQ Sequence 9 AA;

Query Match 77.8%; Score 35; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
 |||||
 Db 3 HLSLRGL 9

RESULT 9

ABJ07543
 ID ABJ07543 standard; Peptide; 9 AA.

XX AC ABJ07543;

XX DT 14-NOV-2002 (first entry)

XX DE Hepatitis B virus epitope #1761.

XX KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 XX virucide; hepatotropic; antiinflammatory.

XX OS Hepatitis B virus.

PN WO200219986-A1.
 XX 14-MAR-2002.
 PD 08-SEP-2000; 2000WO-US24802.
 PF 08-SEP-2000; 2000WO-US24802.
 PR 08-SEP-2000; 2000WO-US24802.
 XX (EPIM-) EPIMUNE INC.
 PA (SETT/) SETTE A.
 XX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 PI Celis E, Kubo RT, Grey HM, Chesnut RW;
 XX WPI; 2002-643192/69.
 DR Vaccine composition for treating or preventing hepatitis B virus (HBV)
 XX infection, and/or for stimulating an immune response to HBV, comprises
 PT a HBV peptide epitope -
 PT
 XX
 PS Disclosure; Page 146; 228pp; English.
 XX
 CC The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention.
 XX
 SQ Sequence 9 AA;
 Query Match 77.8%; Score 35; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HLSLRGL 7
 DB 2 HLSLRGL 8
 RESULT 11
 ABJ09377
 ID ABJ09377 standard; Peptide; 9 AA.
 XX
 AC ABJ09377;
 XX
 DT 14-NOV-2002 (first entry)
 XX
 DE Hepatitis B virus epitope #3565.
 XX
 KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 KW virucide; hepatotropic; antiinflammatory.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200219986-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 08-SEP-2000; 2000WO-US24802.
 XX
 PR 08-SEP-2000; 2000WO-US24802.
 XX
 PA (EPIM-) EPIMUNE INC.
 PA (SETT/) SETTE A.
 XX
 PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 PI Celis E, Kubo RT, Grey HM, Chesnut RW;
 XX
 DR WPI; 2002-643192/69.
 XX
 PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
 PT infection, and/or for stimulating an immune response to HBV, comprises
 PT a HBV peptide epitope -
 XX
 PS Disclosure; Page 186; 228pp; English.
 XX
 CC The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention.
 XX
 SQ Sequence 9 AA;
 Query Match 77.8%; Score 35; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HLSLRGL 7
 DB 2 HLSLRGL 8
 RESULT 10
 ABJ09365
 ID ABJ09365 standard; Peptide; 9 AA.
 XX
 AC ABJ09365;
 XX
 DT 14-NOV-2002 (first entry)
 XX
 DE Hepatitis B virus epitope #3553.
 XX
 KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 KW virucide; hepatotropic; antiinflammatory.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200219986-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 08-SEP-2000; 2000WO-US24802.
 XX
 PR 08-SEP-2000; 2000WO-US24802.
 XX
 PA (EPIM-) EPIMUNE INC.
 PA (SETT/) SETTE A.
 XX
 PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 PI Celis E, Kubo RT, Grey HM, Chesnut RW;
 XX
 DR WPI; 2002-643192/69.
 XX
 PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
 PT infection, and/or for stimulating an immune response to HBV, comprises
 PT a HBV peptide epitope -
 XX

CC The present invention relates to a composition comprising at least one
CC hepatitis B virus epitope. This can be used in the production of a
CC vaccine for use in preventing or treating hepatitis B virus infection.
CC The present sequence is a peptide described in the exemplification of the
CC invention.

XX
SQ Sequence 11 AA;

Query Match 77.8%; Score 35; DB 23; Length 11;
Best Local Similarity 100.0%; Pred.No. 0.99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
| | | | |
Db 1 HLSLRGL 7

RESULT 15

ABJ07119
ID ABJ07119 standard; Peptide; 11 AA.

XX
AC ABJ07119;

DT 14-NOV-2002 (first entry)

DE Hepatitis B virus epitope #1337.

KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
KW virucide; hepatotropic; antiinflammatory.

OS Hepatitis B virus.

PN WO200219986-A1.

PD 14-MAR-2002.

PF 08-SEP-2000; 2000WO-US24802.

PR 08-SEP-2000; 2000WO-US24802.

PA (EPIM-) EPIMUNE INC.

PA (SETT/) SETTE A.

PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
PI Celis E, Kubo RT, Grey HW, Chesnut RW;

XX WPI; 2002-643192/69.

XX Vaccine composition for treating or preventing hepatitis B virus (HBV)
PT infection, and/or for stimulating an immune response to HBV, comprises
PT a HBV peptide epitope -

PS Disclosure; Page 136; 228pp; English.

CC The present invention relates to a composition comprising at least one
CC hepatitis B virus epitope. This can be used in the production of a
CC vaccine for use in preventing or treating hepatitis B virus infection.
CC The present sequence is a peptide described in the exemplification of the
CC invention.

XX
SQ Sequence 11 AA;

Query Match 77.8%; Score 35; DB 23; Length 11;
Best Local Similarity 100.0%; Pred.No. 0.99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
| | | | |
Db 5 HLSLRGL 11

Search completed: December 23, 2003, 08:43:59
Job time : 27.8 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:41:18 , Search time 9.6 Seconds
(without alignments)
39.666 Million cell updates/sec

Title: US-09-989-621-1
Perfect score: 45
Sequence: 1 HSLRGLFV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	4	US-09-051-006-1
2	36	80.0	322	4	US-09-328-352-5489
3	35	77.8	15	4	US-09-009-953-147
4	35	77.8	15	4	US-09-009-953-150
5	35	77.8	19	6	5183734-6
6	35	77.8	20	6	5183734-14
7	35	77.8	153	6	5196194-20
8	35	77.8	153	6	5204446-4
9	35	77.8	154	4	US-09-719-528A-5
10	35	77.8	154	6	5183734-1
11	32	71.1	180	4	US-08-913-159-13
12	32	71.1	377	1	US-07-959-946-1
13	32	71.1	377	1	US-08-333-577-1
14	32	71.1	377	5	PCT-US92-08634-1
15	32	71.1	4536	4	US-09-180-422B-27
16	32	71.1	4563	1	US-09-108-006C-1
17	31	68.9	201	1	US-08-415-751-2
18	31	68.9	257	2	US-08-467-265-16
19	31	68.9	257	3	US-08-467-265-16
20	31	68.9	257	3	US-09-407-891-16
21	31	68.9	308	4	US-09-252-991A-30126
22	31	68.9	351	1	US-08-415-751-17
23	31	68.9	440	4	US-09-077-955-26
24	31	68.9	456	4	US-09-077-955-26
25	31	68.9	492	2	US-08-644-271-32
26	31	68.9	492	4	US-09-077-955-36
27	31	68.9	530	4	US-09-252-991A-23666

28	31	68.9	1156	3	US-08-996-083-1	Sequence 1, Appli
29	31	68.9	1156	3	US-09-429-516-1	Sequence 1, Appli
30	31	68.9	1156	3	US-09-429-516-3	Sequence 3, Appli
31	30	66.7	199	1	US-08-299-162A-2	Sequence 2, Appli
32	30	66.7	199	2	US-08-467-265-14	Sequence 14, Appli
33	30	66.7	199	2	US-08-467-265-17	Sequence 17, Appli
34	30	66.7	199	3	US-08-467-265-14	Sequence 14, Appli
35	30	66.7	199	3	US-08-467-265-17	Sequence 17, Appli
36	30	66.7	199	3	US-09-407-891-14	Sequence 14, Appli
37	30	66.7	199	3	US-09-407-891-17	Sequence 17, Appli
38	30	66.7	371	4	US-09-252-991A-27127	Sequence 27127, A
39	30	66.7	482	4	US-09-252-991A-20932	Sequence 20932, A
40	30	66.7	553	3	US-08-845-546-12	Sequence 12, Appli
41	30	66.7	708	4	US-09-328-352-6131	Sequence 6131, Ap
42	30	66.7	719	4	US-09-252-991A-28768	Sequence 28768, A
43	30	66.7	746	4	US-09-252-991A-29228	Sequence 29228, A
44	29	64.4	13	4	US-09-461-325-525	Sequence 525, App
45	29	64.4	43	4	US-09-227-357-264	Sequence 264, App

ALIGNMENTS

RESULT 1
US-09-051-006-1
; Sequence 1, Application US/09051006
; Patent No. 6380353
; GENERAL INFORMATION:
; APPLICANT: Mogam Biotechnology Research Institute
; APPLICANT: Kim, Tae-Young
; APPLICANT: Lee, Ki-Young
; APPLICANT: Chang, Jin-Soo
; APPLICANT: Cho, Sung-Yoo
; APPLICANT: Hwang, Yu-Kyeong
; APPLICANT: Choi, Myeong
; APPLICANT: Cheong, Hong-Seok
; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
; FILE REFERENCE: 0136/03154
; CURRENT APPLICATION NUMBER: US/09/051,006
; CURRENT FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-051-006-1

Query Match 100.0%; Score 45; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HSLRGLFV 9
DB 1 HSLRGLFV 9

RESULT 2
US-09-328-352-5489
; Sequence 5489, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03FA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5489
; LENGTH: 322
; TYPE: PRT

ORGANISM: Acinetobacter baumannii
US-09-328-352-5489

Query Match 80.0%; Score 36; DB 4; Length 322;
Best Local Similarity 55.6%; Pred. No. 5.5,
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLSLRGLFV 9
Db 7 HIKLRGIFI 15

RESULT 3

US-09-009-953-147

; Sequence 147, Application US/09009953

; Patent No. 6413517

; GENERAL INFORMATION:

; APPLICANT: Sette, Alessandro

; TITLE OF INVENTION: Identification of Broadly

; CORRESPONDENCE ADDRESS: Reactive DR Restricted Epitopes

; NUMBER OF SEQUENCES: 274

; ADDRESS: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/009,953

; FILING DATE: 21-Jan-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/036,713

; FILING DATE: 23-JAN-1997

; APPLICATION NUMBER: US 60/037,432

; FILING DATE: 07-FEB-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Ellen Lauver

; REGISTRATION NUMBER: 32,762

; REFERENCE/DOCKET NUMBER: 018623-011520US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-576-0200

; TELEFAX: 415-576-0300

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 147:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 147:

US-09-009-953-147

Query Match 77.8%; Score 35; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLSLRGL 7
Db 3 HLSLRGL 9

RESULT 4

US-09-009-953-150

; Sequence 150, Application US/09009953

; Patent No. 6413517

GENERAL INFORMATION:

; APPLICANT: Sette, Alessandro

; TITLE OF INVENTION: Identification of Broadly

; CORRESPONDENCE ADDRESS: Reactive DR Restricted Epitopes

; NUMBER OF SEQUENCES: 274

; ADDRESS: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/009,953

; FILING DATE: 21-Jan-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/036,713

; FILING DATE: 23-JAN-1997

; APPLICATION NUMBER: US 60/037,432

; FILING DATE: 07-FEB-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Ellen Lauver

; REGISTRATION NUMBER: 32,762

; REFERENCE/DOCKET NUMBER: 018623-011520US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-576-0200

; TELEFAX: 415-576-0300

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 150:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 150:

US-09-009-953-150

Query Match 77.8%; Score 35; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.27;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLSLRGL 7

Db 1 HLSLRGL 7

RESULT 5

5183734-6

; Patent No. 5183734

; APPLICANT: MORIARTY, ANN M.

; TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS

; FOR ASSAYING SV40 HBXAG

; NUMBER OF SEQUENCES: 17

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/553,982

; FILING DATE: 17-JUL-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 54,424

; FILING DATE: 26-MAY-1987

; APPLICATION NUMBER: 648,142

; FILING DATE: 07-SEP-1984

; APPLICATION NUMBER: 587,570

; FILING DATE: 08-MAR-1984

; SEQ ID NO: 6:

LENGTH: 19

5183734-6

Query Match 77.8%; Score 35; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HLSLRL 7
DB 10 HLSLRL 16

RESULT 6
5183734-14
; Patent No. 5183734
; APPLICANT: MORIARTY, ANN M.
; TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
; FOR ASSAYING SV40 HBXAG
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,982
; FILING DATE: 17-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 54,424
; FILING DATE: 26-MAY-1987
; APPLICATION NUMBER: 648,142
; FILING DATE: 07-SEP-1984
; APPLICATION NUMBER: 587,570
; FILING DATE: 08-MAR-1984
; SEQ ID NO:14:
; LENGTH: 20
5183734-14

Query Match 77.8%; Score 35; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HLSLRL 7
DB 11 HLSLRL 17

RESULT 7
5196194-20
; Patent No. 5196194
; APPLICANT: RUTTER, WILLIAM J.; GOODMAN, HOWARD M.
; TITLE OF INVENTION: VACCINES CONTAINING HEPATITIS B S-PROTEIN
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/679,621
; FILING DATE: 7-DEC-1984
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 513,055
; FILING DATE: 12-JUL-1983
; APPLICATION NUMBER: 107,267
; FILING DATE: 21-DEC-1979
; APPLICATION NUMBER: 41,909
; FILING DATE: 24-MAY-1979
; SEQ ID NO:20:
; LENGTH: 153
5196194-20

Query Match 77.8%; Score 35; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HLSLRL 7
DB 52 HLSLRL 58

RESULT 8
5204446-4
; Patent No. 5204446
; APPLICANT: KUMAZAWA, TOSHIKI; OSANAI, MASATOSHI

; TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY
; WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/503,239
; FILING DATE: 02-APR-1990
; SEQ ID NO:4:
; LENGTH: 153
5204446-4

Query Match 77.8%; Score 35; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRL 7
DB 52 HLSLRL 58

RESULT 9
US-09-719-528A-5
; Sequence 5, Application US/09719528A
; Patent No. 6558675
; GENERAL INFORMATION:
; APPLICANT: Oom, Chong Jin
; Lim, Gek Keow
; Zhao, Yi
; Chen, Wei Ning
; TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
; USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61 Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/719,528A
FILING DATE: 30-Apr-2001
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SG98/00046
FILING DATE: 19-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Mass, Clifford J.
REGISTRATION NUMBER: 30,086
REFERENCE/DOCKET NUMBER: U-013109-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 708-1800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-719-528A-5

Query Match 77.8%; Score 35; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HLSLRL 7
DB 52 HLSLRL 58

RESULT 10
 5183734-1
 ; PATENT NO. 5183734
 ; APPLICANT: MORIARTY, ANN M.
 ; TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
 ; FOR ASSAYING SV40 HBXAG
 ; NUMBER OF SEQUENCES: 17
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/553,982
 ; FILING DATE: 17-JUL-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 54,424
 ; FILING DATE: 26-MAY-1987
 ; APPLICATION NUMBER: 648,142
 ; FILING DATE: 07-SEP-1984
 ; APPLICATION NUMBER: 587,570
 ; FILING DATE: 08-MAR-1984
 ; SEQ ID NO:1
 ; LENGTH: 154
 5183734-1

Query Match 77.8%; Score 35; DB 6; Length 154;
 Best Local Similarity 100.0%; Pred. No. 3.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLSLRGL 7
 Db 52 HLSLRGL 58
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RESULT 11
 US-08-913-159-13
 ; Sequence 13, Application US/08913159
 ; Patent No. 6300109
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: Plasmid-derived type II
 ; TITLE OF INVENTION: restriction-modification systems from Lactococcus lactis
 ; NUMBER OF SEQUENCES: 14
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30 (BFO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/913,159
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DK 0179/95
 ; FILING DATE: 17-FEB-1995
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 180 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-913-159-13

Query Match 71.4%; Score 32; DB 4; Length 180;
 Best Local Similarity 66.7%; Pred. No. 21;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLSLRGLFV 9
 Db 148 HVSLSLFLV 156
 |||||

RESULT 12
 US-07-959-946-1
 ; Sequence 1, Application US/07959946
 ; Patent No. 5408038
 ; GENERAL INFORMATION:

APPLICANT: Smith, Richard K.
 APPLICANT: Koduri, Raju
 APPLICANT: Young, Stephen G.
 APPLICANT: Witstum, Joseph L.
 APPLICANT: Curtiss, Linda K.
 TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
 TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Goldsmith, Shore, Suker &
 ADDRESSEE: Milnamow, Ltd.
 STREET: 180 No. 5408038th Stetson, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/959,946
 FILING DATE: 19921008
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,706
 FILING DATE: 18-JUN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Gamson, Edward P.
 REGISTRATION NUMBER: 29,381
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 616-5400
 TELEFAX: (312) 616-5460
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 377 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-959-946-1

Query Match 71.1%; Score 32; DB 1; Length 377;
 Best Local Similarity 75.0%; Pred. No. 49;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HLSLRGLF 8
 Db 330 HLQLEGLF 337
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RESULT 13
 US-08-333-577-1
 ; Sequence 1, Application US/08333577
 ; Patent No. 5786206
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith, Richard K.
 ; APPLICANT: Koduri, Raju
 ; APPLICANT: Young, Stephen G.
 ; APPLICANT: Witstum, Joseph L.
 ; APPLICANT: Curtiss, Linda K.
 ; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
 ; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Goldsmith, Shore, Suker &
 ; ADDRESSEE: Milnamow, Ltd.
 ; STREET: 180 No. 5786206th Stetson, Suite 4700
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60601


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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,577
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: SCRF 234.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-333-577-1
Query Match 71.1%; Score 32; DB 1; Length 377;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HLSLRGLF 8
DB 330 HLQLEGLF 337

RESULT 14
PCT-US92-08634-1
; Sequence 1, Application PC/TUS9208634
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Witatum, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milnarcw, Ltd.
; STREET: 180 North Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/08634
; FILING DATE: 19921009
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,706
; FILING DATE: 18-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
PCT-US92-08634-1
Query Match 71.1%; Score 32; DB 5; Length 377;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HLSLRGLF 8
DB 330 HLQLEGLF 337

RESULT 15
US-09-180-422B-27
; Sequence 27, Application US/09180422B
; Patent No. 644644
; GENERAL INFORMATION:
; APPLICANT: BRUCKDORFER, KARL R
; ETELAIE, CAMILLE
; TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED
; FROM APOLIPOPROTEIN B-100
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE, P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/180,422B
; FILING DATE: 07-Dec-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36663
; REFERENCE/DOCKET NUMBER: 117-268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4536 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-180-422B-27
Query Match 71.1%; Score 32; DB 4; Length 4536;
Best Local Similarity 75.0%; Pred. No. 8.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HLSLRGLF 8
DB 3543 HLQLEGLF 3550

Search completed: December 23, 2003, 08:53:45
Job time : 11.6 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:40:03 ; Search time 79.4 Seconds
(without alignments)
21.169 Million cell updates/sec

Title: US-09-989-621-1

Perfect score: 45

Sequence: 1 HLSRLGLFV 9

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Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	10	US-09-989-621-1
2	37	82.2	1436	11	Sequence 1, Appli
3	37	82.2	1436	14	Sequence 448, App
4	35	77.8	154	15	Sequence 78, Appli
5	33	73.3	224	10	Sequence 5, Appli
6	33	73.3	224	12	Sequence 1537, Ap
7	33	73.3	526	15	Sequence 23, Appl
8	33	73.3	864	12	Sequence 1, Appli
9	32	71.1	430	9	Sequence 395, App
10	32	71.1	1871	12	Sequence 442, App
11	32	71.1	1906	12	Sequence 114, App
12	32	71.1	4563	10	Sequence 88, Appl
13	32	71.1	4563	11	Sequence 128, App
14	32	71.1	4563	12	Sequence 32, Appl
15	31	68.9	53	12	Sequence 128, App
					Sequence 31587, A

16	68.9	74	9	US-09-764-869-787	Sequence 787, App
17	68.9	74	15	US-10-091-504-787	Sequence 787, App
18	68.9	196	12	US-09-946-290-10	Sequence 10, Appl
19	68.9	257	10	US-09-911-346-16	Sequence 16, Appl
20	68.9	257	12	US-10-408-766-21	Sequence 21, Appl
21	68.9	440	14	US-10-016-283-26	Sequence 26, Appl
22	68.9	456	14	US-10-016-283-25	Sequence 25, Appl
23	68.9	492	14	US-10-016-283-36	Sequence 36, Appl
24	68.9	616	15	US-10-156-761-14772	Sequence 14772, A
25	68.9	1156	9	US-09-757-716-1	Sequence 1, Appli
26	66.7	66	9	US-09-764-869-1076	Sequence 1076, Ap
27	66.7	66	15	US-10-091-504-1076	Sequence 1076, Ap
28	66.7	131	11	US-09-895-298-100	Sequence 100, App
29	66.7	198	11	US-09-202-329-13	Sequence 13, Appl
30	66.7	199	10	US-09-911-346-14	Sequence 14, Appl
31	66.7	199	10	US-09-911-346-17	Sequence 17, Appl
32	66.7	199	12	US-10-205-194-53	Sequence 53, Appl
33	66.7	233	9	US-09-925-301-973	Sequence 973, App
34	66.7	237	9	US-09-813-242-10964	Sequence 10964, A
35	66.7	237	15	US-10-260-877-46	Sequence 46, Appl
36	66.7	506	15	US-10-053-192-4	Sequence 4, Appli
37	66.7	552	12	US-10-094-749-3253	Sequence 3253, Ap
38	66.7	553	15	US-10-225-567A-520	Sequence 520, App
39	66.7	1709	15	US-10-156-761-11180	Sequence 11180, A
40	64.4	13	15	US-10-012-542-525	Sequence 525, App
41	64.4	43	11	US-09-983-802-264	Sequence 264, App
42	64.4	103	11	US-10-106-698-5482	Sequence 5482, Ap
43	64.4	110	9	US-09-764-891-4907	Sequence 4907, Ap
44	64.4	128	15	US-09-867-550-328	Sequence 328, App
45	64.4	128	15	US-10-128-714-3068	Sequence 3068, Ap

ALIGNMENTS

Handwritten: us-09-989-621-1

RESULT 1

US-09-989-621-1
; Sequence 1, Application US/09989621
; Patent No. US20030151683A1
; GENERAL INFORMATION:
; APPLICANT: Mogam Biotechnology Research Institute
; APPLICANT: Kim, Tae-Young
; APPLICANT: Lee, Ki-Young
; APPLICANT: Chang, Jin-Soo
; APPLICANT: Cho, Sung-Yoo
; APPLICANT: Hwang, Yu-Kyeong
; APPLICANT: Choi, Myeong
; APPLICANT: Cheong, Hong-Seok
; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
; TITLE OF INVENTION: Derived from X Protein of Hepatitis B virus
; FILE REFERENCE: 0136/05154
; CURRENT APPLICATION NUMBER: US/09/989, 621
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/051,006
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-989-621-1

Query Match 100.0%; Score 45; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HLSRLGLFV 9

DB 1 HLSRLGLFV 9

RESULT 2

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US-09-759-130B-448
; Sequence 448, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kist, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MP100-5350MIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; PRIOR FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 448
; LENGTH: 1436
; TYPE: PRT
; ORGANISM: Bovine
US-09-759-130B-448

Query Match      82.2%; Score 37; DB 11; Length 1436;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 HLSLRGLFV 9
Db 6 HLSLRGLCV 14

RESULT 3
US-10-042-431-78
; Sequence 78, Application US/10042431
; Publication No. US20020182675A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Sean A
; APPLICANT: BARNES, Thomas M
; APPLICANT: FRASER, Christopher C
; APPLICANT: SHARP, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
; FILE REFERENCE: 10147-612
; CURRENT APPLICATION NUMBER: US/10/042,431
; CURRENT FILING DATE: 2001-10-25

US-09-759-130B-448
; Sequence 448, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kist, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MP100-5350MIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; PRIOR FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 448
; LENGTH: 1436
; TYPE: PRT
; ORGANISM: Bovine
US-09-759-130B-448

Query Match      82.2%; Score 37; DB 11; Length 1436;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 HLSLRGLFV 9
Db 6 HLSLRGLCV 14

RESULT 3
US-10-042-431-78
; Sequence 78, Application US/10042431
; Publication No. US20020182675A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Sean A
; APPLICANT: BARNES, Thomas M
; APPLICANT: FRASER, Christopher C
; APPLICANT: SHARP, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
; FILE REFERENCE: 10147-612
; CURRENT APPLICATION NUMBER: US/10/042,431
; CURRENT FILING DATE: 2001-10-25

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; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/578,063
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 1436
; TYPE: PRT
; ORGANISM: Bos sp.
US-10-042-431-78

Query Match      82.2%; Score 37; DB 14; Length 1436;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLSLRGLFV 9
Db 6 HLSLRGLCV 14

RESULT 4
US-10-209-264-5
; Sequence 5, Application US/10209264
; Publication No. US20030003111A1
; GENERAL INFORMATION:
; APPLICANT: Oon, Chong Jin
; APPLICANT: Lim, Gek Keow
; APPLICANT: Zhao, Yi
; APPLICANT: Chen, Wei Ning
; TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61 Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/209,264
; FILING DATE: 31-Jul-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/SG98/00046
; FILING DATE: 19-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J.
; REGISTRATION NUMBER: 30,086
; REFERENCE/DOCKET NUMBER: U-013109-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 154 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-209-264-5

Query Match      77.8%; Score 35; DB 15; Length 154;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLSLRGL 7
Db 1 HLSLRGL 7

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Db 52 HSLRLCL 58

RESULT 5

US-09-925-300-1537
 ; Sequence 1537, Application US/09925300
 ; Patent No. US20020151681A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Craig Rosen,
 ; APPLICANT: Steve Ruben,
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA101
 ; CURRENT APPLICATION NUMBER: US/09/925,300
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05988
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1890
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1537
 ; LENGTH: 224
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-925-300-1537

Query Match 73.3%; Score 33; DB 10; Length 224;
 Best Local Similarity 75.0%; Pred. No. 70;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSLRGLFV 9

Db 149 LALRGLFI 156

RESULT 6

US-10-408-766-23
 ; Sequence 23, Application US/10408766
 ; Publication No. US20030228294A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Chi
 ; APPLICANT: Wensev, Diane
 ; TITLE OF INVENTION: INHIBITION OF TUMOR GROWTH VIA
 ; FILE REFERENCE: PEROXIDEDOXIN 3
 ; CURRENT APPLICATION NUMBER: US/10/408,766
 ; CURRENT FILING DATE: 2003-04-08
 ; PRIOR APPLICATION NUMBER: 60/370,873
 ; PRIOR FILING DATE: 2002-04-08
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 23
 ; LENGTH: 256
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-408-766-23

Query Match 73.3%; Score 33; DB 12; Length 256;
 Best Local Similarity 75.0%; Pred. No. 81;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSLRGLFV 9

Db 181 LALRGLFI 188

RESULT 7

US-10-053-192-1
 ; Sequence 1, Application US/10053192
 ; Publication No. US20030087336A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BACHMANN, Heinrich
 ; APPLICANT: BRUGGER, Roland

; APPLICANT: FRIEDLEIN, Arno M
 ; APPLICANT: WIRTZ, Gabriele M
 ; APPLICANT: WOGGON, Wolf-Dietrich
 ; APPLICANT: WYSS, Adrian
 ; APPLICANT: WYSS, Markus
 ; TITLE OF INVENTION: BETA,BETA-CAROTENE 15,15'-DIOXYGENASES, NUCLEIC ACID
 ; FILE REFERENCE: SEQUENCES CODING THEREFOR AND THEIR USE
 ; FILE REFERENCE: B-B-CAROTENE 15,15'-DIOXYGENASES,...
 ; CURRENT APPLICATION NUMBER: US/10/053,192
 ; CURRENT FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 103382.0
 ; PRIOR FILING DATE: 1999-02-22
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 526
 ; TYPE: PRT
 ; ORGANISM: CHICKEN
 US-10-053-192-1

Query Match 73.3%; Score 33; DB 15; Length 526;
 Best Local Similarity 55.6%; Pred. No. 1.7e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HSLRGLFV 9

Db 508 HLDLRGNFI 516

RESULT 8

US-10-238-075-395
 ; Sequence 395, Application US/10238075
 ; Publication No. US20030148324A1
 ; GENERAL INFORMATION:
 ; APPLICANT: I.N.S.E.R.M.
 ; TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat
 ; FILE REFERENCE: BLANDINE
 ; CURRENT APPLICATION NUMBER: US/10/238,075
 ; CURRENT FILING DATE: 2002-09-10
 ; PRIOR APPLICATION NUMBER: 0003145
 ; PRIOR FILING DATE: 2000-03-10
 ; NUMBER OF SEQ ID NOS: 1576
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 395
 ; LENGTH: 864
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 US-10-238-075-395

Query Match 73.3%; Score 33; DB 12; Length 864;
 Best Local Similarity 62.5%; Pred. No. 3e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HSLRGLF 8

Db 776 HIGIRGLF 783

RESULT 9

US-09-741-669-442
 ; Sequence 442, Application US/09741669
 ; Patent No. US20020022718A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Forsyth, R. Allyn
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; TITLE OF INVENTION: Genes identified as required for
 ; FILE REFERENCE: Proliferation of E. coli
 ; FILE REFERENCE: ELITRA.009A
 ; CURRENT APPLICATION NUMBER: US/09/741,669
 ; CURRENT FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: US 60/173005

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; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 442
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-741-669-442

Query Match 71.1%; Score 32; DB 9; Length 430;
Best Local Similarity 55.6%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLSLRGLFV 9
Db 151 HLSLRGIVL 159

RESULT 10
US-10-144-194A-114
; Sequence 114, Application US/10144194A
; Publication No. US20030215809A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies Inc
; TITLE OF INVENTION: Regulated Breast Cancer Genes
; FILE REFERENCE: 3U 103 R1
; CURRENT APPLICATION NUMBER: US/10/144,194A
; CURRENT FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 114
; LENGTH: 1871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-194A-114

Query Match 71.1%; Score 32; DB 12; Length 1871;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLSLRGLFV 9
Db 342 HLSLRPIFL 350

RESULT 11
US-10-144-194A-88
; Sequence 88, Application US/10144194A
; Publication No. US20030215809A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies Inc
; TITLE OF INVENTION: Regulated Breast Cancer Genes
; FILE REFERENCE: 3U 103 R1
; CURRENT APPLICATION NUMBER: US/10/144,194A
; CURRENT FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88
; LENGTH: 1906
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-194A-88

Query Match 71.1%; Score 32; DB 12; Length 1906;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLSLRGLFV 9
Db 377 HLSLRPIFL 385

RESULT 12
US-10-144-194A-114
; Sequence 114, Application US/10144194A
; Publication No. US20030215809A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies Inc
; TITLE OF INVENTION: Regulated Breast Cancer Genes
; FILE REFERENCE: 3U 103 R1
; CURRENT APPLICATION NUMBER: US/10/144,194A
; CURRENT FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 114
; LENGTH: 1871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-194A-114

Query Match 71.1%; Score 32; DB 12; Length 1871;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLSLRGLFV 9
Db 342 HLSLRPIFL 350

RESULT 13
US-09-802-640-32
; Sequence 32, Application US/09802640
; Publication No. US20030036057A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bonsel Aruna
; APPLICANT: Klevy Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: 24736-2048
; CURRENT APPLICATION NUMBER: US/09/802,640
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 4563
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-802-640-32

Query Match 71.1%; Score 32; DB 11; Length 4563;
Best Local Similarity 75.0%; Pred. No. 2.8e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HLSLRGLF 8
Db 3570 HLQLEGLF 3577

RESULT 14
US-09-751-708A-128
; Sequence 128, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: Tervan, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128

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; LENGTH: 4563
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-751-708A-128

Query Match      71.1%; Score 32; DB 12; Length 4563;
Best Local Similarity 75.0%; Pred. No. 2.8e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HSLRGLF 8
Db 3570 HLQLEGLF 3577

RESULT 15
US-10-029-386-31587
; Sequence 31587, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: ACONICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 31587
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008985.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.8
; OTHER INFORMATION: SWISSPROT HIT: Q54513, EVALUE 6.20e+00
US-10-029-386-31587

Query Match      68.9%; Score 31; DB 12; Length 53;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HSLRGL 7
Db 28 HLELRGL 34

Search completed: December 23, 2003, 08:52:48
Job time : 80.4 secs
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GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.
 CM protein - protein search, using sw model
 Run on: December 23, 2003, 08:40:03 ; Search time 79.4 Seconds
 (without alignments)
 21.169 Million cell updates/sec

Title: US-09-989-621-2
 Perfect score: 45
 Sequence: 1 VLHKRTGL 9
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA.*
 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 2: /cgn2_6/ptodata/1/pubpaa/PTC_NEW_PUB.pep.*
 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 6: /cgn2_6/ptodata/1/pubpaa/PTCUS_PUBCOMB.pep.*
 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	9	10	US-09-989-621-2
2	39	86.7	154	15	US-10-209-264-5
3	34	75.6	293	12	US-10-427-442-12
4	34	75.6	691	12	US-10-258-165-254
5	33	73.3	630	11	US-09-938-795A-1
6	32	71.1	403	15	US-10-156-761-10822
7	32	71.1	448	9	US-09-815-242-10596
8	32	71.1	748	9	US-09-815-242-10278
9	32	71.1	748	9	US-09-815-242-13880
10	32	71.1	869	9	US-09-815-242-5230
11	32	71.1	882	9	US-09-815-242-12526
12	31	68.9	23	14	US-10-001-870-215
13	31	68.9	65	15	US-10-050-704-148
14	31	68.9	72	15	US-10-050-704-307
15	31	68.9	320	9	US-09-872-153-22

16	31	68.9	320	16	US-10-176-306-20	Sequence 20, Appl
17	31	68.9	369	12	US-09-954-342-8	Sequence 8, Appl
18	31	68.9	369	12	US-09-954-342-12	Sequence 12, Appl
19	31	68.9	390	12	US-09-944-049-20	Sequence 20, Appl
20	31	68.9	412	12	US-09-944-049-22	Sequence 22, Appl
21	31	68.9	422	12	US-09-954-342-10	Sequence 10, Appl
22	31	68.9	424	10	US-09-843-905A-13	Sequence 13, Appl
23	31	68.9	424	12	US-10-317-250-13	Sequence 13, Appl
24	31	68.9	483	12	US-10-029-386-32939	Sequence 32939, A
25	31	68.9	734	15	US-10-054-683-19	Sequence 19, Appl
26	31	68.9	734	15	US-10-205-823-10	Sequence 10, Appl
27	31	68.9	735	15	US-10-205-823-8	Sequence 8, Appl
28	31	68.9	753	15	US-10-205-823-6	Sequence 6, Appl
29	30	66.7	84	12	US-10-340-578-54	Sequence 54, Appl
30	30	66.7	239	14	US-10-076-785-36	Sequence 36, Appl
31	30	66.7	265	11	US-09-866-050A-655	Sequence 655, App
32	30	66.7	303	9	US-09-765-272-202	Sequence 202, App
33	30	66.7	328	12	US-09-769-744A-48	Sequence 48, Appl
34	30	66.7	340	9	US-09-815-242-10736	Sequence 10736, A
35	30	66.7	376	10	US-09-882-872-2	Sequence 2, Appl
36	30	66.7	414	12	US-10-063-735-102	Sequence 102, App
37	30	66.7	414	12	US-10-199-672-314	Sequence 314, App
38	30	66.7	414	12	US-10-187-749-314	Sequence 314, App
39	30	66.7	414	12	US-10-194-457-314	Sequence 314, App
40	30	66.7	414	12	US-10-184-642-314	Sequence 314, App
41	30	66.7	414	12	US-10-196-747-314	Sequence 314, App
42	30	66.7	414	12	US-10-173-689-314	Sequence 314, App
43	30	66.7	414	12	US-10-173-690-314	Sequence 314, App
44	30	66.7	414	12	US-10-173-691-314	Sequence 314, App
45	30	66.7	414	12	US-10-173-692-314	Sequence 314, App

ALIGNMENTS

RESULT 1

US-09-989-621-2
 ; Sequence 2, Application US/09989621
 ; Patent No. US20020151683A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mogam Biotechnology Research Institute
 ; APPLICANT: Kim, Tae-Young
 ; APPLICANT: Lee, Ki-Young
 ; APPLICANT: Chang, Jin-Soo
 ; APPLICANT: Cho, Sung-Yoo
 ; APPLICANT: Hwang, Yu-Kyeong
 ; APPLICANT: Choi, Myeong
 ; APPLICANT: Cheong, Hong-Seok
 ; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
 ; FILE REFERENCE: Derived from X Protein of Hepatitis B virus
 ; FILE REFERENCE: 0136/OE154
 ; CURRENT APPLICATION NUMBER: US/09/989,621
 ; CURRENT FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: 09/051,006
 ; PRIOR FILING DATE: 2000-11-17
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Hepatitis B virus
 ; US-09-989-621-2

Query Match 100.0%; Score 45; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.2e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VLHKRTGL 9

Db 1 VLHKRTGL 9

RESULT 2

US-10-209-264-5

; Sequence 5, Application US/10209264
; Publication No. US20030003111A1
; GENERAL INFORMATION:
; APPLICANT: Oon, Chong Jin
; Lim, Gek Keow
; Zhao, Yi
; Chen, Wei Ning

TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
USSES THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ladas & Parry

STREET: 26 West 61 Street

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10023

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/209,264

FILING DATE: 31-Jul-2002

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/SG98/00046

FILING DATE: 19-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Mass, Clifford J.

REGISTRATION NUMBER: 30,086

REFERENCE/DOCKET NUMBER: U-013109-7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 708-1800

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 154 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-209-264-5

Query Match 86.7%; Score 39; DB 15; Length 154;

Best Local Similarity 88.9%; Pred. No. 3.4;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 5

Db 92 VLYKRTLGL 100

RESULT 3

US-10-427-442-12

; Sequence 12, Application US/10427442

; Publication No. US2003017523A1

; GENERAL INFORMATION:

; APPLICANT: Falco, Carl

; APPLICANT: Famodu, Omolayo O.

; APPLICANT: Kinney, Tony

; APPLICANT: Rafalski, Antoni

TITLE OF INVENTION: Phosphatidylcholine Biosynthetic Enzyme

CURRENT APPLICATION NUMBER: US/10/427,442

PRIOR FILING DATE: 2003-05-01

PRIOR APPLICATION NUMBER: US/09/668,262A

PRIOR FILING DATE: 2000-09-22

PRIOR APPLICATION NUMBER: 60/155626

PRIOR FILING DATE: 1999-09-23

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Microsoft Office 95

; SEQ ID NO 12

; LENGTH: 293

; TYPE: PRT

; ORGANISM: Zea mays

US-10-427-442-12

Query Match 75.6%; Score 34; DB 12; Length 293;

Best Local Similarity 75.0%; Pred. No. 67;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHKRTLGL 9

Db 208 LHRTLGV 215

RESULT 4

US-10-259-165-254

; Sequence 254, Application US/10259165

; Publication No. US2003013588A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Tong

; APPLICANT: Wang, Xun

; APPLICANT: Chang, Hur-song

; APPLICANT: Briggs, Steven P.

; APPLICANT: Cooper, Bret

; APPLICANT: Glazebrook, Jane

; APPLICANT: Goff, Stephen A.

; APPLICANT: Katagiri, Fumiyaki

; APPLICANT: Kreps, Joel

; APPLICANT: Moughamer, Todd

; APPLICANT: Provart, Nicholas

; APPLICANT: Ricke, Darrell

TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING

FILE REFERENCE: 70030-NP

CURRENT APPLICATION NUMBER: US/10/259,165

PRIOR FILING DATE: 2002-09-26

PRIOR APPLICATION NUMBER: US 60/370,620

PRIOR FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: US 60/368,327

PRIOR FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: US 60/325,277

PRIOR FILING DATE: 2001-09-26

NUMBER OF SEQ ID NOS: 782

SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta

SEQ ID NO 254

LENGTH: 691

TYPE: PRT

ORGANISM: Oryza sativa

FEATURE:

NAME/KEY: X region

LOCATION: (278)..(278)

OTHER INFORMATION: Xaa = any naturally occurring amino acid

US-10-259-165-254

Query Match

Best Local Similarity

Matches

QY

Db

RESULT 5

US-09-938-795A-1

; Sequence 1, Application US/09938795A

; Publication No. US2003004568A1

; GENERAL INFORMATION:

; APPLICANT: CHU, CHARLES CHIYUAN

; APPLICANT: CHAVAN, SANGEETA S.

; APPLICANT: MASON, JAMES M.

TITLE OF INVENTION: HUMAN INTERLEUKIN-FOUR INDUCED PROTEIN

FILE REFERENCE: LIJ-9000-US


```

; CURRENT APPLICATION NUMBER: US/09/938,795A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227,818
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Mus sp.
JS-09-938-795A-1

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Query Match 73.3%; Score 33; DB 11; Length 630;
Best Local Similarity 72.7%; Pred.No. 2.3e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

```

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2Y 1 VLHK--RTLGL 9
   :||| :|||
3B 122 ILHKLRTLGL 132

```

```

RESULT 6
JS-10-156-761-10822
; Sequence 10822, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10822
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
JS-10-156-761-10822

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Query Match 71.1%; Score 32; DB 15; Length 403;
Best Local Similarity 55.6%; Pred.No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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2Y 1 VLHKRTLGL 9
   :||| :|||
3B 81 VHNQTLGI 89

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RESULT 7
JS-09-815-242-10596
; Sequence 10596, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A

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; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10596
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10596

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Query Match 71.1%; Score 32; DB 9; Length 448;
Best Local Similarity 55.6%; Pred.No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VLHKRTLGL 9
   :||| :|||
DB 263 VIHEKSLGL 271

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```

RESULT 8
US-09-815-242-10278
; Sequence 10278, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10278
; LENGTH: 748
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-815-242-10278

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Query Match 71.1%; Score 32; DB 9; Length 748;
 Best Local Similarity 85.7%; Pred. No. 4.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHRTLG 7
 |||:||||
 Db 378 VLHRTLG 384

RESULT 9
 US-09-815-242-13880
 ; Sequence 13880, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; Prokaryotes
 ; FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 1410
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13880
 ; LENGTH: 748
 ; TYPE: PRT
 ; ORGANISM: Salmonella typhi
 US-09-815-242-13880

Query Match 71.1%; Score 32; DB 9; Length 748;
 Best Local Similarity 85.7%; Pred. No. 4.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHRTLG 7
 |||:||||
 Db 378 VLHRTLG 384

RESULT 10
 US-09-815-242-5230
 ; Sequence 5230, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; Prokaryotes

FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 1410
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5230
 ; LENGTH: 869
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-815-242-5230

Query Match 71.1%; Score 32; DB 9; Length 869;
 Best Local Similarity 62.5%; Pred. No. 5.2e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHRTLG 8
 |||:||||
 Db 569 ILHRTVG 576

RESULT 11
 US-09-815-242-12526
 ; Sequence 12526, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; Prokaryotes
 ; FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 1410
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12526
 ; LENGTH: 882
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-815-242-12526

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Query Match          71.1%; Score 32; DB 9; Length 882;
Best Local Similarity 62.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHKRTLG 8
DB 582 ILHKRVVG 589

RESULT 12
US-10-001-870-215
; Sequence 215, Application US/10001870
; Publication No. US20020150924A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Hervé
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
; FILE REFERENCE: DEX-0283
; CURRENT APPLICATION NUMBER: US/10/001,870
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,189
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 215
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-870-215

Query Match          68.9%; Score 31; DB 14; Length 23;
Best Local Similarity 56.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
DB 8 VVEKRTLGL 16

RESULT 13
US-10-050-704-148
; Sequence 148, Application US/10050704
; Publication No. US20030050442A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/050,704
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 148
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-704-148

Query Match          68.9%; Score 31; DB 15; Length 65;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 2 LHKRTLG 8
DB 58 LHPRTLGL 64

RESULT 14
US-10-050-704-307
; Sequence 307, Application US/10050704
; Publication No. US20030050442A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/050,704
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 307
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-704-307

Query Match          68.9%; Score 31; DB 15; Length 72;
Best Local Similarity 85.7%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LHKRTLG 8
DB 65 LHPRTLGL 71

RESULT 15
US-09-872-153-22
; Sequence 22, Application US/09872153
; Patent No. US20020082207A1
; GENERAL INFORMATION:
; APPLICANT: Hirst, Shannon K.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Dillon, Devin C.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.531
; CURRENT APPLICATION NUMBER: US/09/872,153
; CURRENT FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-153-22

Query Match          68.9%; Score 31; DB 9; Length 320;
Best Local Similarity 75.0%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHKRTLG 8
DB 146 VLHQRTCLG 153

Search completed: December 23, 2003, 08:52:48
Job time : 79.4 secs
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GenCore version 5.1.6
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DM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 11 Seconds
(without alignments)
78.683 Million cell updates/sec

Title: US-09-989-621-2

Perfect score: 45

Sequence: 1 VLHKRTLGL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 76:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	45	100.0	134	1 B48345	gene X protein, tr
2	45	100.0	154	1 QQVLD1	gene X protein - h
3	45	100.0	154	1 QQVLBH	gene X protein - h
4	45	100.0	154	1 A48345	gene X protein - h
5	45	100.0	154	1 QQVLA1	gene X protein - h
6	45	100.0	154	1 QQVLAW	gene X protein - h
7	45	100.0	154	1 QQVLKS	gene X protein - h
8	45	100.0	154	1 QQVLCP	gene X protein - h
9	45	100.0	154	2 S20756	gene X protein - h
10	45	100.0	154	2 S47404	gene X protein - h
11	45	100.0	154	2 S47408	gene X protein - h
12	45	100.0	154	2 JS0256	gene X protein - h
13	45	100.0	154	2 S67503	gene X protein - h
14	45	100.0	154	2 JQ2228	trans-activating p
15	45	100.0	154	2 S25650	gene X protein - h
16	45	100.0	154	2 S53130	gene X protein - h
17	45	100.0	154	2 JS0603	gene X protein - h
18	45	100.0	154	2 JS0604	gene X protein - h
19	45	100.0	154	2 S33687	gene X protein - h
20	45	100.0	154	2 S12542	gene X protein - h
21	45	100.0	154	2 S32203	gene X protein - h
22	45	100.0	154	2 S22319	gene X protein - h
23	45	100.0	154	2 S20751	gene X protein - h
24	45	100.0	154	2 T13466	gene X protein - h
25	45	100.0	359	2 S04570	gene X/C fusion pr
26	42	93.3	154	2 S35529	gene X protein - h
27	42	93.3	172	2 A58456	X protein - human
28	39	86.7	210	2 T13472	gene X protein - h
29	39	86.7	210	2 S12598	gene X protein - h

pyruvate kinase-li
pyruvate kinase-li
n-acetylglucosamin
probable ribosomal
hypothetical prote
hypothetical prote
probable polyketid
clipB protein VC071
lysine decarboxyla
ATPases with chape
class III stressor
SmpB protein PA476
phosphoribosylglyc
hypothetical prote
erythronate-4-phos
erythronate-4-phos

ALIGNMENTS

RESULT 1

B48345
gene X protein, truncated form - hepatitis B virus

C:Species: hepatitis B virus, HBV

C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999

C:Accession: B48345

R:Repp, R.; Keller, C.; Borkhardt, A.; Csecke, A.; Schaefer, S.; Gerlich, W.H.; Lampert,

Arch. Virol. 125, 299-304, 1992

A>Title: Detection of a hepatitis B virus variant with a truncated X gene and enhancer I)

A:Reference number: A48345; MUID:92352333; PMID:1642555

A:Accession: B48345

A:Molecule type: DNA

A:Residues: 1-134 <REP>

A:Cross-references: GB:S41176; NID:G252541; PIDN:AAB22733.1; PID:G252542

A:Note: sequence extracted from NCBI backbone (NCBIN:109914, NCBIP:109915)

C:Genetics:

A:Gene: X

C:Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 45; DB 1; Length 134;

Best Local Similarity 100.0%; Pred. No. 0.036;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHKRTLGL 9

Db 92 VLHKRTLGL 100

RESULT 2

QQVLD1

gene X protein - hepatitis B virus (subtype aYW)

C:Species: hepatitis B virus, HBV

C>Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 08-Apr-1994

C:Accession: A03719

R:Galibert, F.; Mandart, E.; Fitoussi, P.; Tiollais, P.; Charnay, P.

Nature 281, 646-650, 1979

A>Title: Nucleotide sequence of the hepatitis B virus genome (subtype aYW) in E. coli.

A:Reference number: A93214; MUID:81012091; PMID:399327

A:Accession: A03719

A:Molecule type: DNA

A:Residues: 1-154 <GAL>

A:Cross-references: GB:J02203; GB:V01460

C:Genetics:

A:Gene: X

C:Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 45; DB 1; Length 154;

Best Local Similarity 100.0%; Pred. No. 0.042;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHKRTLGL 9

Db 92 VLHKRTLGL 100

Db 92 VLHRTGL 100

RESULT 3

QOVLBH
Gene X protein - hepatitis B virus (subtype ayw, strain PHB320)
C/Species: hepatitis B virus, HBV
A/Variety: subtype ayw, strain PHB320
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Jul-2000
C/Accession: A05237; S53144; S53173; S53195; S53210; S53217; S53222; S53224; S53235; S53280

Ribicko, V.; Pushko, P.; Dragalina, D.; Pumpen, P.; Gren, E.
FEBS Lett. 185, 208-212, 1985
A/Title: Subtype ayw variant of hepatitis B virus: DNA primary structure analysis.
A/Reference number: A05237; NUID:85204397; PMID:3996597

A/Accession: A05237
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-154 <BIC>
A/Cross-references: EMBL:X02496; NID:G62280; PIDN:CAB41697.1; PID:G4704317
A/Experimental source: subtype ayw, strain PHB320
Rilal, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995

A/Reference number: S5312
A/Accession: S53144
A/Molecule type: DNA
A/Residues: 124-154 <LAI>
A/Cross-references: EMBL:X85267; NID:G736025; PIDN:CAA59548.1; PID:G736026; EMBL:X85284; S5305; EMBL:X85307; EMBL:X85308; EMBL:X85310; EMBL:X85312; EMBL:X85313; EMBL:X85315; EMBL:X85316
A/Experimental source: isolate patient Pintus '85 et al.

A/Accession: S53173
A/Molecule type: DNA
A/Residues: 124-154 <LA2>
A/Cross-references: EMBL:X85277; NID:G736065; PIDN:CAA59575.1; PID:G736066
A/Experimental source: isolate patient Bio'90
C/Genetics:
A/Genes: X
C/Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHRTGL 9
| | | | |
Db 92 VLHRTGL 100

RESULT 4

A48345
Gene X protein - hepatitis B virus
C/Species: hepatitis B virus, HBV
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C/Accession: A48345
R. Repp, R.; Keller, C.; Borkhardt, A.; Csecke, A.; Schaefer, S.; Gerlich, W.H.; Lampert, Arch. Virol. 125, 299-304, 1992
A/Title: Detection of a hepatitis B virus variant with a truncated X gene and enhancer I
A/Reference number: A48345; NUID:52352333; PMID:1642555

A/Accession: A48345
A/Molecule type: DNA
A/Residues: 1-154 <REP>
A/Cross-references: GB:S41175; NID:G252539; PIDN:AAB2732.1; PID:G252540
A/Note: sequence extracted from NCBI backbone (NCBIN:109912, NCBIF:109913)
C/Genetics:
A/Genes: X
C/Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHRTGL 9
| | | | |

Db 92 VLHRTGL 100

RESULT 5

QOVLAI
Gene X protein - hepatitis B virus (strain alpha1)
C/Species: hepatitis B virus, HBV
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C/Accession: D34773
R/Tong, S.; Li, J.; Vitvitski, L.; Trepo, C.
Virology 176, 595-603, 1990

A/Title: Active hepatitis B virus replication in the presence of anti-HBe is associated
A/Reference number: A34773; NUID:90266476; PMID:2345966
A/Accession: D34773
A/Status: translation not shown
A/Molecule type: DNA

A/Residues: 1-154 <TON>
A/Cross-references: EMBL:M32138; NID:G329667; PIDN:AAA45504.1; PID:G329671
C/Genetics:
A/Genes: X
C/Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHRTGL 9
| | | | |
Db 92 VLHRTGL 100

RESULT 6

QOVLAW
Gene X protein - hepatitis B virus (subtype adw and adw2)
C/Species: hepatitis B virus, HBV
C/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 30-Jun-1998
C/Accession: A31289; B94409; X03719
R/Lo, S.J.; Chien, M.L.; Lee, Y.H.W.
Virology 167, 289-292, 1988
A/Title: Characteristics of the X gene of hepatitis B virus.
A/Reference number: A31289; NUID:89045656; PMID:3188399

A/Accession: A31289
A/Molecule type: DNA
A/Residues: 1-154 <LOS>
A/Experimental source: subtype adw
R/Valenzuela, P.; Quiroga, M.; Zaldivar, J.; Gray, P.; Rutter, W.J.
in Animal Virus Genetics, Field, B.N., Jaenisch, R., and Fox, C.F., eds., pp.57-70, Acad
A/Reference number: A94409

A/Accession: B94409
A/Molecule type: DNA
A/Residues: 1-154 <VAL>
A/Experimental source: subtype adw2
C/Genetics:
A/Genes: X
C/Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHRTGL 9
| | | | |
Db 92 VLHRTGL 100

RESULT 7

QOVLKS
Gene X protein - hepatitis B virus (subtype adw, strain 991)
C/Species: hepatitis B virus, HBV
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C/Accession: S10380
R/Koeschel, H.G.; Schueler, A.; Lottmann, S.; Thomsen, R.
submitted to the EMBL Data Library, February 1990

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A;Reference number: S10380
A;Accession: S10380
A;Molecule type: DNA
A;Residues: 1-154 <KOE>
A;Cross-references: EMBL:X51970; NID:g1155012; PIDN:CAA36231.1; PID:g60432
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
    |||||
Db 92 VLHKRTLGL 100

RESULT 8
QQVLCF
gene X protein - hepatitis B virus (strain LSH, chimpanzee)
C;Species: hepatitis B virus, HBV
C;Date: 30-Jun-1999 #sequence_revision 30-Jun-1989 #text_change 16-Jun-2000
C;Accession: D28885
R;Vaadin, M.; Wolstenholme, A.J.; Tsiquaye, K.N.; Zuckerman, A.J.; Harrison, T.J.
J. Gen. Virol. 69, 1383-1389, 1988
A;Title: The complete nucleotide sequence of the genome of a hepatitis B virus isolated
A;Reference number: A92796; MUID:88258473; PMID:2838576
A;Accession: D28885
A;Molecule type: DNA
A;Residues: 1-154 <VAU>
A;Cross-references: GB:D00220; NID:G221505; PIDN:BAA00160.1; PID:G221509
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ZY 1 VLHKRTLGL 9
    |||||
Db 92 VLHKRTLGL 100

RESULT 9
S20756
gene X protein - hepatitis B virus (subtype ayw, patient E)
C;Species: hepatitis B virus, HBV
A;Variety: subtype ayw, patient E
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C;Accession: S20756
R;Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Melis, A.; Porru, A.
submitted to the EMBL Data Library, March 1992
A;Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negative
A;Reference number: S20745
A;Accession: S20756
A;Molecule type: DNA
A;Residues: 1-154 <LAI>
A;Cross-references: EMBL:X65259; NID:G59439; PIDN:CAA46360.1; PID:G59443
A;Experimental source: subtype ayw, patient E
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 45; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ZY 1 VLHKRTLGL 9
    |||||
Db 92 VLHKRTLGL 100

RESULT 10
S47404
gene X protein - hepatitis B virus (subtype ayw4)
C;Species: hepatitis B virus, HBV
A;Variety: subtype ayw4
C;Date: 23-Nov-1994 #sequence_revision 12-May-1995 #text_change 26-Aug-1999
C;Accession: S47404
R;Plucieniczak, A.
submitted to the EMBL Data Library, August 1994
A;Description: Molecular cloning and sequencing of two complete genomes of polish isolate
A;Reference number: S47404
A;Accession: S47404
A;Molecule type: DNA
A;Residues: 1-154 <PLU>
A;Cross-references: EMBL:Z35716; NID:G527435; PIDN:CAA84785.1; PID:G527436
A;Experimental source: subtype ayw4
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 45; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
    |||||
Db 92 VLHKRTLGL 100

RESULT 11
S47408
gene X protein - hepatitis B virus (subtype adw2)
C;Species: hepatitis B virus, HBV
A;Variety: subtype adw2
C;Date: 23-Nov-1994 #sequence_revision 12-May-1995 #text_change 26-Aug-1999
C;Accession: S47408
R;Plucieniczak, A.
submitted to the EMBL Data Library, August 1994
A;Description: Molecular cloning and sequencing of two complete genomes of polish isolate
A;Reference number: S47404
A;Accession: S47408
A;Molecule type: DNA
A;Residues: 1-154 <PLU>
A;Cross-references: EMBL:Z35717; NID:G527440; PIDN:CAA84789.1; PID:G527441
A;Experimental source: subtype adw2
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 45; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
    |||||
Db 92 VLHKRTLGL 100

RESULT 12
JS0256
gene X protein - hepatitis B virus (subtype adw, strain Japan/pUDW233)
C;Species: hepatitis B virus, HBV
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 14-Nov-1997
C;Accession: JS0256
R;Okamoto, H.; Tada, F.; Sakagawa, H.; Saetsoeewignjo, R.I.; Imai, M.; Miyakawa, Y.; Ma
J. Gen. Virol. 69, 2575-2583, 1988
A;Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of surf
A;Reference number: JS0253; MUID:89010694; PMID:3171552
A;Accession: JS0256
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-154 <OKA>
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A;Cross-references: GB:D00329; NID:9221497

C;Genetics:

A;Gene: X

C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 45; DB 2; Length 154;

Best Local Similarity 100.0%; Pred. No. 0.042;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9

|||||

Db 92 VLHKRTLGL 100

RESULT 13

S67503

Gene X protein - hepatitis B virus (subtype ayw3, isolate Hope CH1357)

C;Species: hepatitis B virus, HBV

A;Variety: subtype ayw3, isolate Hope CH1357

C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 26-Aug-1999

C;Accession: S67503

R;Order: H.; Ebert, J.W.; Fields, H.A.; Mushahwar, I.K.; Magnus, L.O.

Virology 218, 214-223, 1996

A;Title: Complete sequencing of a gibbon hepatitis B virus genome reveals a unique genot

A;Reference number: S67503; MUID:96207410; PMID:8615024

A;Accession: S67503

A;Molecule type: DNA

A;Residues: 1-154 <NA>

A;Cross-references: EMBL:U46935; NID:G1814218; PIDN:AA841949.1; PID:G1814219

A;Experimental source: subtype ayw3, isolate Hope CH1357

C;Genetics:

A;Gene: X

C;Superfamily: hepatitis B virus gene X protein

Query Match

Best Local Similarity 100.0%; Score 45; DB 2; Length 154;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9

|||||

Db 92 VLHKRTLGL 100

RESULT 14

JQ2228

trans-activating protein X - hepatitis B virus

N;Alternate names: HBx protein

C;Species: hepatitis B virus, HBV

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 26-Aug-1999

C;Accession: JQ2228; S31794

R;Naumann, H.; Schaefer, S.; Yoshida, C.F.T.; Gaspar, A.M.C.; Repp, R.; Gerlich, W.H.

J. Gen. Virol. 74, 1627-1632, 1993

A;Title: Identification of a new hepatitis B virus (HBV) genotype from Brazil that expe

A;Reference number: JQ2228; MUID:93346970; PMID:8345355

A;Accession: JQ2228

A;Molecule type: DNA

A;Residues: 1-154 <NA>

A;Cross-references: EMBL:X69798; NID:G59422; PIDN:CAA49453.1; PID:G59424

C;Superfamily: hepatitis B virus gene X protein

Query Match

Best Local Similarity 100.0%; Score 45; DB 2; Length 154;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9

|||||

Db 92 VLHKRTLGL 100

RESULT 15

S25650

gene X protein - hepatitis B virus (subtype ayw, patient D)

C;Species: hepatitis B virus, HBV

A;Variety: subtype ayw, patient D

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C;Accession: S25650

R;Lai, M.Z.; Mazzoleni, A.P.; Melis, A.; Balestrieri, A.

submitted to the EMBL Data Library, September 1992

A;Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negati

A;Reference number: S25650

A;Accession: S25650

A;Molecule type: DNA

A;Residues: 1-154 <LAI>

A;Cross-references: EMBL:X68292; NID:G59448; PIDN:CAA48352.1; PID:G59449

A;Experimental source: subtype ayw, patient D

C;Genetics:

A;Gene: X

C;Superfamily: hepatitis B virus gene X protein

Query Match

Best Local Similarity 100.0%; Score 45; DB 2; Length 154;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9

|||||

Db 92 VLHKRTLGL 100

Search completed: December 23, 2003, 08:41:05

Job time : 12 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 6.4 Seconds
(without alignments)
66.131 Million cell updates/sec

Title: US-09-989-621-2

Perfect score: 45

Sequence: 1 VLHKRTLGL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	154	1 X_HPBV2	P03166 hepatitis b
2	45	100.0	154	1 X_HPBV4	P12936 hepatitis b
3	45	100.0	154	1 X_HPBV9	P17102 hepatitis b
4	45	100.0	154	1 X_HPBVA	P24026 hepatitis b
5	45	100.0	154	1 X_HPBVI	P20975 hepatitis b
6	45	100.0	154	1 X_HPBVI	P20976 hepatitis b
7	45	100.0	154	1 X_HPBVL	P12912 hepatitis b
8	45	100.0	154	1 X_HPBVL	P20977 hepatitis b
9	45	100.0	154	1 X_HPBVT	P05499 hepatitis b
10	45	100.0	154	1 X_HPBVI	P03165 hepatitis b
11	35	77.8	144	1 RL28_DROME	Q9VZS5 drosophila
12	35	77.8	147	1 RL13_MYCTU	O06260 mycobacteri
13	34	75.6	273	1 DLH1_YEAST	Q07505 saccharomyc
14	33	73.3	630	1 FIG1_MOUSE	Q09045 mus musculu
15	32	71.1	151	1 CV53_DICDI	Q23894 dictyosteli
16	32	71.1	159	1 SRP_PSEAE	Q8V40 pseudomonas
17	32	71.1	160	1 SRP_AZOMI	Q8K14 azotobacter
18	32	71.1	249	1 Y361_SYNY3	Q55578 synechocyst
19	32	71.1	748	1 PTIP_ECOLI	P37177 escherichia
20	32	71.1	748	1 PTIP_SALTY	P37178 salmonella
21	31	68.9	121	1 RNL2_CHICK	P81476 gallus galli
22	31	68.9	268	1 Y739_MYCTU	O53802 mycobacteri
23	31	68.9	390	1 UL13_HCMVA	P16849 human cytom
24	31	68.9	461	1 GPL3_YEAST	P32363 saccharomyc
25	31	68.9	498	1 YAC3_CAEPO	Q09817 schizosacch
26	31	68.9	532	1 ERA2_CABEL	Q21353 caenorhabdi
27	31	68.9	655	1 YJHG_ECOLI	P39358 escherichia
28	31	68.9	735	1 AD02_HUMAN	Q39965 homo sapien
29	31	68.9	815	1 AXH_HAEIN	P44505 haemophilus
30	31	68.9	1828	1 MY5A_RAT	Q9GY13 rattus norv
31	30	66.7	231	1 RADC_BACSU	Q02170 bacillus su
32	30	66.7	294	1 BLAC_CITDI	P22390 citrobacter
33	30	66.7	360	1 ARG1_XENLA	Q91553 xenopus lae

Q91554 xenopus lae
Q91555 xenopus lae
Q9PJH4 chlamydia t
Q46449 chlamydia t
P08458 saccharomyc
P12374 pseudomonas
P44403 haemophilus
P46523 brassica na
P30190 trypanosoma
O61078 leishmania
P27570 crithidia f
O88974 mus musculu

34 30 66.7 360 1 ARG2_XENLA
35 30 66.7 360 1 ARG3_XENLA
36 30 66.7 377 1 RPOA_CHLMU
37 30 66.7 377 1 RPOA_CHLTR
38 30 66.7 490 1 SPS1_YEAST
39 30 66.7 609 1 CLPB_HAEIN
40 30 66.7 856 1 CLPB_BRANA
41 30 66.7 874 1 CLPB_BRANA
42 30 66.7 1232 1 TOP2_TRYCR
43 30 66.7 1236 1 TOP2_LEICH
44 30 66.7 1239 1 TOP2_CRIFA
45 30 66.7 1307 1 SETB_MOUSE

ALIGNMENTS

RESULT 1

X_HPBV2
ID X_HPBV2 STANDARD; PRT; 154 AA.
AC P03166; P12935;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw2), and
OS Hepatitis B virus (subtype adw).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
CX NCBI_TaxID=10408, 106821;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=ADW2;
RA Valenzuela P., Quiroga M., Zaldivar J., Gray P., Rutter W.J.;
RL (In) Field B.N., Jaenisch R., Fox C.F. (eds.);
RL Animal virus genetics, pp.57-70, Academic Press, New York (1980).
[2]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=ADM;
RA MEDLINE=89045656; PubMed=3188399;
RT Lo S.O., Chien M.L., Lee Y.H.W.;
RL "Characteristics of the X gene of hepatitis B virus.";
RL Virology 167:289-292(1988).
[3]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=ADM;
RA MEDLINE=83168919; PubMed=6300776;
RT Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;
RL "The complete nucleotide sequences of the cloned hepatitis B virus
DNA; subtype adr and adw.";
RL Nucleic Acids Res. 11:1747-1757(1983).
[4]
RN
RP FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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EMBL; X02763; CAA26540.1; -
EMBL; Z35717; CAA84789.1; -
DR EMBL; M23692; AAA56820.1; -
DR EMBL; V00866; -; NOT_ANNOTATED_CDS.
DR PIR; A31289; QOVLAW.
DR PIR; S47408; S47408.
DR InterPro; IPR000236; Transactx.
DR Pfam; PF00739; X; 1.
FT CONFLICT 80 80 E -> A (IN REF. 3).
FT CONFLICT 115 115 C -> S (IN REF. 2).
FT CONFLICT 130 131 KV -> MI (IN REF. 3).
FT CONFLICT 154 AA; 16593 MW; 7F2AE32A4F025670 CRC64;
SQ SEQUENCE

```

Query Match      100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTGL 9
   |||||
Db 92 VLHKRTGL 100

RESULT 2
X_HPBVA
ID X_HPBV4 STANDARD; PRT; 154 AA.
AC P12936;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adr4).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10409;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83246570; PubMed=6306594;
RA Fujiyama A., Miyachara A., Nozaki C., Yoneyama T., Ohtono N.,
RA Matsubara K.;
RT "cloning and structural analyses of hepatitis B virus DNAs, subtype
RT adr.";
RL Nucleic Acids Res. 11:4601-4610(1983).
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CC -----
DR EMBL; X01587; CAA25744.1; -
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 15622 MW; 594A1D0718928804 CRC64;

Query Match      100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTGL 9
   |||||
Db 92 VLHKRTGL 100

RESULT 3
X_HPBV9
ID X_HPBV9 STANDARD; PRT; 154 AA.
AC P17102;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adr / strain 991).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10410;
RN [1]
RP SEQUENCE FROM N.A.
RA Koechel H.G., Schueler A., Lottmann S., Thomssen R.;
RA Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; X51970; CAA36231.1; -
DR PIR; S10380; QOVLKS.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16553 MW; 52A0D9CFE6DCDE0 CRC64;

Query Match      100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTGL 9
   |||||
Db 92 VLHKRTGL 100

RESULT 4
X_HPBVA
ID X_HPBVA STANDARD; PRT; 154 AA.
AC P24026;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (strain alpha1).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10411;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90266476; PubMed=2345966;
RA Tong S., Li J., Vitvitski L., Trepo C.;
RT "Active hepatitis B virus replication in the presence of anti-HBe is
RT associated with viral variants containing an inactive pre-C region.";
RL Virology 176:596-603(1990).
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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CC -----
DR EMBL; M32138; AAA45504.1; -
DR PIR; D34773; QOVLAL.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16671 MW; 2CFEEA77FA5E271F CRC64;

Query Match      100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTGL 9
   |||||
Db 92 VLHKRTGL 100

RESULT 5
X_HPBVI
ID X_HPBVI STANDARD; PRT; 154 AA.
AC P20975;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)

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DE Trans-activating protein X.
DS Hepatitis B virus (subtype adw / strain Indonesia/pIDW420).
SC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
DX NCBI_TaxID=10412;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
LA Okamoto H., Tsuda F., Sakugawa H., Sastrosowigno R.I., Imai M.,
LA Miyakawa Y., Mayumi M.;
LA "Typing hepatitis B virus by homology in nucleotide sequence:
LA comparison of surface antigen subtypes.";
LA J. Gen. Virol. 69:2575-2583(1988).
LA -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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LA -----
LA EMBL; D00331; -; NOT_ANNOTATED_CDS.
LA PIR; JS0604; JS0604.
LA InterPro; IPR000236; TransactX.
LA Pfam; PF00739; X; 1.
LA SEQUENCE 154 AA; 16585 MW; C90C817E961BFEB9 CRC64;
LA -----
LA Query Match 100.0%; Score 45; DB 1; Length 154;
LA Best Local Similarity 100.0%; Pred. No. 0.024;
LA Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
LA -----
LA 1 VLHKRTGL 9
LA |||||
LA 92 VLHKRTGL 100
LA -----
LA RESULT 6
LA X HPBVJ STANDARD; PRT; 154 AA.
LA ID X HPBVJ
LA AC P20376;
LA DT 01-FEB-1991 (Rel. 17, Created)
LA DT 01-FEB-1991 (Rel. 17, Last sequence update)
LA DT 01-NOV-1995 (Rel. 32, Last annotation update)
LA DE Trans-activating protein X.
LA GN X.
LA OS Hepatitis B virus (subtype adw / strain Japan/pJDNW233).
LA OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
LA OX NCBI_TaxID=10413;
LA [1]
LA SEQUENCE FROM N.A.
LA MEDLINE=89010694; PubMed=3171552;
LA Okamoto H., Tsuda F., Sakugawa H., Sastrosowigno R.I., Imai M.,
LA Miyakawa Y., Mayumi M.;
LA "Typing hepatitis B virus by homology in nucleotide sequence:
LA comparison of surface antigen subtypes.";
LA J. Gen. Virol. 69:2575-2583(1988).
LA -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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LA -----
LA EMBL; D00329; -; NOT_ANNOTATED_CDS.
LA PIR; JS0256; JS0256.
LA InterPro; IPR000236; TransactX.
LA Pfam; PF00739; X; 1.
LA SEQUENCE 154 AA; 16585 MW; 512A5A077169D5CA CRC64;
LA -----

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Query Match 100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VLHKRTGL 9
DB 92 VLHKRTGL 100
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RESULT 7
X HPBVL STANDARD; PRT; 154 AA.
ID X HPBVL
AC P2912;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (strain lsh / chimpanzee isolate).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10414;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=88258473; PubMed=2838576;
LA Vaadin M., Woldstenholme A.J., Tsiquaye K.N., Zuckerman A.J.,
LA Harrison T.J.;
LA "The complete nucleotide sequence of the genome of a hepatitis B
LA virus isolated from a naturally infected chimpanzee.";
LA J. Gen. Virol. 69:1383-1389(1988).
LA CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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LA -----
LA EMBL; D00220; BAA00160.1; -
LA PIR; D28885; QVQLCP.
LA InterPro; IPR000236; TransactX.
LA Pfam; PF00739; X; 1.
LA SEQUENCE 154 AA; 16759 MW; F6C9D7D30C16D743 CRC64;
LA -----
Query Match 100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
-----
QY 1 VLHKRTGL 9
DB 92 VLHKRTGL 100
-----
RESULT 8
X HPBVO STANDARD; PRT; 154 AA.
ID X HPBVO
AC P20977;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw / strain Okinawa/pODW282).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10415;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
LA Okamoto H., Tsuda F., Sakugawa H., Sastrosowigno R.I., Imai M.,
LA Miyakawa Y., Mayumi M.;
LA "Typing hepatitis B virus by homology in nucleotide sequence:

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RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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CC -----
DR EMBL; D00330; -; NOT_ANNOTATED_CDS.
DE PIR; J50603; J50603.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16558 MW; E2646C059A30125F CRC64;

Query Match 100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
DB 92 VLHKRTLGL 100

RESULT 9
X_HPBVT STANDARD; PRT; 154 AA.
AC Q05499;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw4 / strain Brazil / isolate w4B).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=45410;
RX MEDLINE=93346970; PubMed=8345355;
RA Naumann H., Schaefer S., Yoshida C.F.T., Gaspar A.M.C., Repp R.,
RA Gerlich W.H.;
RT that expresses HBV surface antigen subtype adw4.;
RL J. Gen. Virol. 74:1627-1632(1993).
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CC -----
DR EMBL; X69798; CAA49453.1; -;
DE PIR; JQ2228; JQ2228.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16715 MW; E523C051B9B0B737 CRC64;

Query Match 100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
DB 92 VLHKRTLGL 100

RESULT 10

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X_HPBVT STANDARD; PRT; 154 AA.
AC P03165;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype ayw).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10418;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012091; PubMed=399327;
RA Galibert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.;
RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)
RT cloned in E. coli.";
RL Nature 281:646-650(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85204397; PubMed=3996597;
RA Bichko V., Dreilina D., Pushko P.M., Pumpen P.P., Gren E.;
RT "Subtype ayw variant of hepatitis B virus. DNA primary structure
RT analysis.";
RL FEBS Lett. 185:208-212(1985).
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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CC -----
DR EMBL; V01460; -; NOT_ANNOTATED_CDS.
DE EMBL; X02496; CAB41697.1; -;
DR PIR; A03719; QQVLD1.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT VARIANT 46 46 P -> S (IN STRAIN LATVIA).
FT VARIANT 84 88 NAHOI -> KAQPF (IN STRAIN LATVIA).
FT VARIANT 102 102 A -> V (IN STRAIN LATVIA).
FT CONFLICT 26 26 R -> C (IN REF. 1).
SQ SEQUENCE 154 AA; 16618 MW; 29FD1CC9E09A34B5 CRC64;

Query Match 100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
DB 92 VLHKRTLGL 100

RESULT 11
RL28 DROME STANDARD; PRT; 144 AA.
AC Q9VZ55;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 60S ribosomal protein L28.
GN CG12740.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.

```

STRAIN=Berkeley; MEDLINE=20196006; PubMed=10731132;
 Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benton P.V., Berhan B.P., Bhandari D., Bolshakov S.,
 Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferrier A., Fleischmann W.,
 Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 Glueck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J.R., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wasserman D.A., Weissstock G.M., Weissbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W.N., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 "The genome sequence of *Drosophila melanogaster*."
 Science 287:2185-2195(2000).
 [2]
 SEQUENCE FROM N.A.
 STRAIN=Berkeley; TISSUE=Embryo;
 MEDLINE=22426066; PubMed=12537569;
 Stapleton M., Carlson J.W., Brockstein P., Yu C., Champe M.,
 George R.A., Guarin H., Kronmiller B., Pacle J.M., Park S., Wan K.H.,
 Rubin G.M., Celisner S.E.;
 "A *Drosophila* full-length cDNA resource."
 Genome Biol. 3:RESEARCH080.1-RESEARCH080.8(2002).
 -!- SIMILARITY: BELONGS TO THE L28E FAMILY OF RIBOSOMAL PROTEINS.

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 EMBL; AE003477; AAF47742.1; --
 EMBL; AF071444; AAL49066.1; --
 FlyBase; FBgn0035422; CG12740.
 GO; GO:0005842; Cytosolic large ribosomal subunit (sensu Eu. .); ISS.
 GO; GO:0003735; F-actin structural constituent of ribosome; ISS.
 GO; GO:0006412; P:protein biosynthesis; ISS.
 InterPro; IPR002672; Ribosomal_L28e.
 Pfam; PF01778; Ribosomal_L28e; 1.
 ProDom; PD010767; Ribosomal_L28e; 1.
 Ribosomal protein.
 KW RIBOSOMAL protein; Complete proteome.
 SQ SEQUENCE 144 AA; 16029 MW; 14D5C7866F585113 CRC64;
 Query Match 77.8%; Score 35; DB 1; Length 144;
 Best Local Similarity 55.6%; Pred. No. 2.9;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLHKRTGL 9
 Db 47 IVHKRTGLV 55
 ID MYCTU STANDARD; PRT; 147 AA.
 RL13 MYCTU
 AC 006250;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 50S ribosomal protein L13.
 GN RPLM OR RV3443C OR MT3548 OR MTCY77.15C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=H37RV;
 MEDLINE=98295987; PubMed=9634230;
 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 Raddock K., Basham D., Brown D., Chillingworth T., Connor R.,
 Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 Rutter S., Seeger K., Skelton J., Squares S., Squares R.,
 Sulston J.E., Taylor K., Whitehead S., Barrett B.G.,
 "Deciphering the biology of *Mycobacterium tuberculosis* from the
 complete genome sequence."
 Nature 393:537-544(1998).
 [2]
 SEQUENCE FROM N.A.
 STRAIN=CDC 1551 / Oshkosh;
 Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 Peterson J.F., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 Bishai W.;
 "Whole genome comparison of *Mycobacterium tuberculosis* clinical and
 laboratory strains."
 Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 -!- FUNCTION: THIS PROTEIN IS ONE OF THE EARLY ASSEMBLY PROTEINS OF
 THE 50S RIBOSOMAL SUBUNIT (BY SIMILARITY).
 -!- SIMILARITY: BELONGS TO THE L13P FAMILY OF RIBOSOMAL PROTEINS.

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 EMBL; Z95389; CAB08692.1; --
 EMBL; AE007159; AAK47889.1; --
 PIR; A70977; A70977.
 TIGR; MT3548; --
 InterPro; IPR005823; L13_bact org.
 InterPro; IPR005822; Rib_prot_L13.
 Pfam; PF00572; Ribosomal_L13; 1.
 ProDom; PD001791; L13_bact org; 1.
 TIGRFAMS; TIGR01066; rplm_bact; 1.
 TRFAMS; TIGR01066; rplm_bact; 1.
 DR PSORT; PS00783; RIBOSOMAL_L13; FALSE NEG.
 KW RIBOSOMAL protein; Complete proteome.
 SQ SEQUENCE 147 AA; 16337 MW; 0D2B2622D62B626 CRC64;
 Query Match 77.8%; Score 35; DB 1; Length 147;

Best Local Similarity 85.7%; Pred. No. 3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHKRTLG 8
Db 84 LHKRTIG 90

RESULT 13
DLHH YEAST STANDARD; PRT; 273 AA.
AC Q07505; (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative carboxymethylenebutenolide (EC 3.1.1.45) (Dienelactone hydrolase) (DLH).
CN YDL086W.
CS Saccharomycetes cerevisiae (Baker's yeast).
CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
CX NCBI_TaxID=4932;
RN SEQUENCE FROM N.A.
RP Wamburt R., Wedler H., Wedler E., Scharfe M.;
RA Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RL
CC -1- CATALYTIC ACTIVITY: 4-carboxymethylenebut-2-en-4-olide + H(2)O = 4
CC -1- OXOHEX-2-enediol.
CC -1- SIMILARITY: BELONGS TO THE DIENELACTONE HYDROLASE FAMILY.
CC
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CC
CC EMBL; Z74134; CAA98652.1; -;
CC PIR; S67622; S67622.
CC SGD; S0002244; YDL086W.
CC InterPro; IPR002925; DLH.
CC Pfam; PF01738; DLH; 1.
KW Hypothetical protein; Hydrolase.
FT ACT_SITE 130 130 BY SIMILARITY.
FT ACT_SITE 191 191 BY SIMILARITY.
FT ACT_SITE 223 223 BY SIMILARITY.
SQ SEQUENCE 273 AA; 30837 MW; 9A4A9B57577243D46 CRC64;
Query Match 75.6%; Score 34; DB 1; Length 273;
Best Local Similarity 75.0%; Pred. No. 9.1;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LHKRTLGL 9
Db 156 IHSRTLGL 163

RESULT 14
FIG1_MOUSE STANDARD; PRT; 630 AA.
AC C09046; Q9CXK7;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-4 induced protein 1 precursor (Fig-1 protein).
GN IL411 OR FIG1.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

STRAIN=CBA/J, and BALB/c;
MEDLINE=97225983; PubMed=9122225;
Chu C.C., Paul W.E.;
"Fig1, an interleukin 4-induced mouse B cell gene isolated by cDNA
representational difference analysis.",
Proc. Natl. Acad. Sci. U.S.A. 94:2507-2512(1997).
[2]
SEQUENCE OF 122-289 FROM N.A.
STRAIN=BALB/c; TISSUE=Spleen;
MEDLINE=99012997; PubMed=9798653;
Chu C.C., Paul W.E.;
"Expressed genes in interleukin-4 treated B cells identified by cDNA
representational difference analysis.",
Mol. Immunol. 35:487-502(1998).
[3]
SEQUENCE OF 217-630 FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Embryonic head;
MEDLINE=21095660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schram L.M., Staali F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.",
Nature 409:685-690(2001).
CC -1- COFACTOR: FAD (POTENTIAL).
CC -1- INDUCTION: By interleukin-4.
CC -1- SIMILARITY: BELONGS TO THE FLAVIN MONOXAMINE OXIDASE FAMILY.
CC STRONG, TO SNAKE L-AMINO ACID OXIDASE.
CC
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CC
CC EMBL; U70429; AAB51353.1; -;
CC EMBL; U70430; AAB51354.1; -;
CC EMBL; U89428; AAC36534.1; -;
CC EMBL; U89429; AAC36535.1; -;
CC EMBL; AK014297; BAB29253.1; ALT_INIT.
CC MGD; MGI:109552; IL411.
CC InterPro; IPR000759; Adrnxd reductase.
CC InterPro; IPR001613; Amineoxid fl.
CC InterPro; IPR002937; Amino oxidase.
CC InterPro; IPR00205; NAD binding.
CC Pfam; PF01593; Amino oxidase; 1.
CC PRINTS; PR00419; ADXRTASE.
CC PRINTS; PR00757; AMINEOXDASEF.
CC Oxidoreductase; Flavoprotein; FAD; Signal.
FT SIGNAL 1 21
FT CHAIN 22 630 INTERLEUKIN-4 INDUCED PROTEIN 1.
FT NP_BIND 59 115 FAD (ADP PART) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 385 385 R -> Q (IN REF. 3).
FT CONFLICT 598 630 PSEHVQVHGEVPEWHGHHGGSGTQMHRVGDHS -> LRSM

YRCMGKSLSGVMGMDLAPRKCTEWGTTTPNRKEEVSTQLLS
QPSGQTDHLH (IN REF. 3).
OPSSQTDHLH; A674C5D6D89A071 CRC64;

Query Match 73.3%; Score 33; DB 1; Length 630;
Best Local Similarity 72.7%; Pred. No. 35;
Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

Y 1 VLHK--RTLGL 9
b 122 ILHKLCTLGL 132

RESULT 15
YS3_DICDI
D_CYS3_DICDI STANDARD; PRT; 151 AA.
C Q23894;
T 01-NOV-1997 (Rel. 35, Created)
T 01-NOV-1997 (Rel. 35, Last sequence update)
T 28-FEB-2003 (Rel. 41, Last annotation update)
E Cysteine proteinase 3 (EC 3.4.22.-) (Cysteine proteinase II)
(Fragment).
E E
N CP3.
S Dictyostelium discoideum (Slime mold).
C Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
X NCBI_TaxID=44689;
IN [1]
IN SEQUENCE FROM N.A.
IP STRAIN=ATCC 24397;
C STRAIN=ATCC 24397;
AT Presse F., Bogdanovsky-Sequeval D., Mathieu M., Felenbok B.;
RT "Structural analysis of a developmentally regulated sequence encoding
IT for a cysteine proteinase in Dictyostelium discoideum.";
Mol. Genet. 203:324-332(1986).
C -!- SUBCELLULAR LOCATION: Lysosomal (Potential).
C -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
C
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C
C EMBL; X03930; CAA27569.1; --
C HSSP; O60911; 1PH0.
C
C DictyDb; D001062; cpxC.
C InterPro; IPR000668; Peptidase_C1.
C InterPro; IPR000169; SHprot_acsite.
C Pfam; PF00112; Peptidase_C1; 1.
C ProDom; PD000158; Peptidase_C1; 1.
C PROSITE; PS00139; THIOLESTERASE_CYS; FALSE NEG.
C PROSITE; PS00639; THIOLESTERASE_HIS; PARTIAL.
C PROSITE; PS00640; THIOLESTERASE_ASN; PARTIAL.
C Hydrolase; Thiol protease; Lysosome.
C NON_TER 1
FT ACT_SITE 100 100 BY SIMILARITY.
FT DISULFID 97 139 BY SIMILARITY.
FT NON_TER 151 151
SQ SEQUENCE 151 AA; 17115 MW; 63952EB5D1A0A6 CRC64;

Query Match 71.1%; Score 32; DB 1; Length 151;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 HKRTLGL 9
Db 61 HKRNGL 67

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M protein - protein search, using sw model

un on: December 23, 2003, 08:39:58 ; Search time 23.6 Seconds
(without alignments)
98.410 Million cell updates/sec

itle: US-09-989-621-2

erfect score: 45

equene: 1 VLHKRTLGL 9

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

earched: 830525 seqs, 258052604 residues

otal number of hits satisfying chosen parameters: 830525

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

SPTREMBL_23.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	45	100.0	60	Q8V787	Q8V787 hepatitis b
2	45	100.0	129	Q8QVU1	Q8QVU1 hepatitis b
3	45	100.0	129	Q8QVU0	Q8QVU0 hepatitis b
4	45	100.0	129	Q8QVU5	Q8QVU5 hepatitis b
5	45	100.0	129	Q8QVU1	Q8QVU1 hepatitis b
6	45	100.0	129	Q8QVU2	Q8QVU2 hepatitis b
7	45	100.0	129	Q8QVU3	Q8QVU3 hepatitis b
8	45	100.0	129	Q8QVU0	Q8QVU0 hepatitis b
9	45	100.0	129	Q8QVU4	Q8QVU4 hepatitis b
10	45	100.0	129	Q8QVU9	Q8QVU9 hepatitis b
11	45	100.0	129	Q8QVU7	Q8QVU7 hepatitis b
12	45	100.0	129	Q8QVU2	Q8QVU2 hepatitis b
13	45	100.0	129	Q8QVU6	Q8QVU6 hepatitis b
14	45	100.0	129	Q8QVU9	Q8QVU9 hepatitis b
15	45	100.0	130	Q91SG7	Q91SG7 hepatitis b
16	45	100.0	130	Q91R67	Q91R67 hepatitis b

17	45	100.0	130	12	Q9DKT3	Q9DKT3 hepatitis b
18	45	100.0	130	12	Q98WJ3	Q98WJ3 hepatitis b
19	45	100.0	130	12	Q9DKT4	Q9DKT4 hepatitis b
20	45	100.0	131	12	Q98WJ2	Q98WJ2 hepatitis b
21	45	100.0	131	12	Q9DKX1	Q9DKX1 hepatitis b
22	45	100.0	134	12	Q91SG6	Q91SG6 hepatitis b
23	45	100.0	134	12	Q9C073	Q9C073 hepatitis b
24	45	100.0	134	12	Q97977	Q97977 hepatitis b
25	45	100.0	134	12	Q9WP86	Q9WP86 hepatitis b
26	45	100.0	134	12	Q9WP53	Q9WP53 hepatitis b
27	45	100.0	134	12	Q98850	Q98850 hepatitis b
28	45	100.0	134	12	Q9DKR0	Q9DKR0 hepatitis b
29	45	100.0	134	12	Q91163	Q91163 hepatitis b
30	45	100.0	134	12	Q91114	Q91114 hepatitis b
31	45	100.0	134	12	Q9WP66	Q9WP66 hepatitis b
32	45	100.0	137	12	O12409	O12409 hepatitis b
33	45	100.0	147	12	Q91SB9	Q91SB9 hepatitis b
34	45	100.0	147	12	Q91SG8	Q91SG8 hepatitis b
35	45	100.0	151	12	Q9DKQ3	Q9DKQ3 hepatitis b
36	45	100.0	151	12	Q9W9S1	Q9W9S1 hepatitis b
37	45	100.0	153	12	Q9YKJ6	Q9YKJ6 hepatitis b
38	45	100.0	153	12	Q9YKJ1	Q9YKJ1 hepatitis b
39	45	100.0	153	12	Q9YKJ8	Q9YKJ8 hepatitis b
40	45	100.0	153	12	Q9YKJ4	Q9YKJ4 hepatitis b
41	45	100.0	154	12	Q94288	Q94288 hepatitis b
42	45	100.0	154	12	Q9J0V0	Q9J0V0 hepatitis b
43	45	100.0	154	12	O09507	O09507 hepatitis b
44	45	100.0	154	12	Q9QXQ5	Q9QXQ5 hepatitis b
45	45	100.0	154	12	Q9GDUH3	Q9GDUH3 hepatitis b

ALIGNMENTS

RESULT 1

Q8V787 ID Q8V787 PRELIMINARY; PRT; 60 AA.
AC Q8V787
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Pre-c protein (Fragment).
GN PRE-C.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=256;
RA Dai E.H., Liu H.J., Song Y.J., Chen C.Y., Wang J., Yang R.F.;
RT "The relationship between mutation of the core promoter and clinical types virus replication in HBV carriers."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067464; EAS84125.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 60 AA; 6879 MW; 9657F85320F96DC1 CRC64;

Query Match Similarity 100.0%; Score 45; DB 12; Length 60;

Best Local Similarity 100.0%; Pred. No. 0.054; 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 1 VLHKRTLGL 9

Db 24 VLHKRTLGL 32

RESULT 2

Q8QVU1 ID Q8QVU1 PRELIMINARY; PRT; 129 AA.
AC Q8QVU1
DT 01-JUN-2002 (T-EMBLrel. 21, Created)

DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE X protein (Fragment).
EN X.
GN Hepatitis B virus.
OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21912118; PubMed=11915040;
RX Kato H., Orito E., Gish R.G., Browej N., Newsom M., Sugauchi F.,
RA Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
RT "Hepatitis B e antigen in sera from individuals from patients with
RL hepatitis B virus of genotype G.";
DR EMBL; AB073437; BAB91088.1; -;
DR Hepatology 35:922-929(2002).
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 129 AA; 13871 MW; 8809A4BE287236F8 CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 VLHKRTLGL 9
| | | | | | | | | |
Db 67 VLHKRTLGL 75

RESULT 3
Q8QVU0 PRELIMINARY; PRT; 129 AA.
ID Q8QVU0
AC Q8QVU0
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE X protein (Fragment).
EN X.
GN Hepatitis B virus.
OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21912118; PubMed=11915040;
RX Kato H., Orito E., Gish R.G., Browej N., Newsom M., Sugauchi F.,
RA Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
RT "Hepatitis B e antigen in sera from individuals from patients with
RL hepatitis B virus of genotype G.";
DR EMBL; AB073438; BAB91089.1; -;
DR Hepatology 35:922-929(2002).
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 129 AA; 13871 MW; 8809A4BE287236F8 CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHKRTLGL 9
| | | | | | | | | |
Db 67 VLHKRTLGL 75

RESULT 4
Q8QVU5 PRELIMINARY; PRT; 129 AA.
ID Q8QVU5
AC Q8QVU5
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE X protein (Fragment).
EN X.
GN Hepatitis B virus.
OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21912118; PubMed=11915040;
RX Kato H., Orito E., Gish R.G., Browej N., Newsom M., Sugauchi F.,
RA Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
RT "Hepatitis B e antigen in sera from individuals from patients with
RL hepatitis B virus of genotype G.";
DR EMBL; AB073439; BAB91090.1; -;
DR Hepatology 35:922-929(2002).
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 129 AA; 13871 MW; 8809A4BE287236F8 CRC64;

GN Hepatitis B virus.
OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21912118; PubMed=11915040;
RX Kato H., Orito E., Gish R.G., Browej N., Newsom M., Sugauchi F.,
RA Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
RT "Hepatitis B e antigen in sera from individuals from patients with
RL hepatitis B virus of genotype G.";
DR EMBL; AB073443; BAB91094.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 129 AA; 13837 MW; 2809A4B42875802E CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHKRTLGL 9
| | | | | | | | | |
Db 67 VLHKRTLGL 75

RESULT 5
Q8QVT1 PRELIMINARY; PRT; 129 AA.
ID Q8QVT1
AC Q8QVT1
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE X protein (Fragment).
EN X.
GN Hepatitis B virus.
OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21912118; PubMed=11915040;
RX Kato H., Orito E., Gish R.G., Browej N., Newsom M., Sugauchi F.,
RA Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
RT "Hepatitis B e antigen in sera from individuals from patients with
RL hepatitis B virus of genotype G.";
DR EMBL; AB073447; BAB91095.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 129 AA; 13825 MW; 31D2F63DF3358031 CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHKRTLGL 9
| | | | | | | | | |
Db 67 VLHKRTLGL 75

RESULT 6
Q8QVU2 PRELIMINARY; PRT; 129 AA.
ID Q8QVU2
AC Q8QVU2
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE X protein (Fragment).
EN X.
GN Hepatitis B virus.
OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21912118; PubMed=11915040;
RX Kato H., Orito E., Gish R.G., Browej N., Newsom M., Sugauchi F.,
RA Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
RT "Hepatitis B e antigen in sera from individuals from patients with
RL hepatitis B virus of genotype G.";
DR EMBL; AB073447; BAB91095.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 129 AA; 13825 MW; 31D2F63DF3358031 CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHKRTLGL 9
| | | | | | | | | |
Db 67 VLHKRTLGL 75

RESULT 6
Q8QVU2 PRELIMINARY; PRT; 129 AA.
ID Q8QVU2
AC Q8QVU2
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE X protein (Fragment).
EN X.
GN Hepatitis B virus.
OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21912118; PubMed=11915040;
RX Kato H., Orito E., Gish R.G., Browej N., Newsom M., Sugauchi F.,
RA Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
RT "Hepatitis B e antigen in sera from individuals from patients with
RL hepatitis B virus of genotype G.";
DR EMBL; AB073447; BAB91095.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 129 AA; 13825 MW; 31D2F63DF3358031 CRC64;

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{ NCBI_TaxID=10407;
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  MEDLINE=21912118; PubMed=11915040;
  SEQUENCE FROM N.A.
  Kato H., Orito E., Gish R.G., Bzowej N., Newsom M., Sugauchi F.,
  Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
  "Hepatitis B e antigen in sera from individuals from patients with
  hepatitis B virus of genotype G.";
  Hepatology 35:922-929(2002).
  EMBL; AB073436; BAB91087.1; -.
  InterPro; IPR000236; TransactX.
  Pfam; PF00739; X; 1.
  NON TER
  SEQUENCE 129 AA; 13837 MW; 8809B55FD863D708 CRC64;
  Query Match 100.0%; Score 45; DB 12; Length 129;
  Best Local Similarity 100.0%; Pred. No. 0.12;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  / 1 VLHKRTLGL 9
  |||||
  67 VLHKRTLGL 75

RESULT 7
SQVT3 PRELIMINARY; PRT; 129 AA.
D Q8QVT3;
I 01-JUN-2002 (TReMBLrel. 21, Created)
I 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
I 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
E X protein (Fragment).
S X.
S Hepatitis B virus.
S Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
X NCBI_TaxID=10407;
[1]
MEDLINE=21912118; PubMed=11915040;
SEQUENCE FROM N.A.
Kato H., Orito E., Gish R.G., Bzowej N., Newsom M., Sugauchi F.,
Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
"Hepatitis B e antigen in sera from individuals from patients with
hepatitis B virus of genotype G.";
Hepatology 35:922-929(2002).
EMBL; AB073445; BAB91096.1; -.
InterPro; IPR000236; TransactX.
Pfam; PF00739; X; 1.
NON TER
SEQUENCE 129 AA; 13837 MW; 2809A4B42875802E CRC64;
Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  / 1 VLHKRTLGL 9
  |||||
  67 VLHKRTLGL 75

RESULT 8
SQVT0 PRELIMINARY; PRT; 129 AA.
D Q8QVT0;
I 01-JUN-2002 (TReMBLrel. 21, Created)
I 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
I 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
E X protein (Fragment).
S X.
S Hepatitis B virus.
S Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
X NCBI_TaxID=10407;
[1]
SEQUENCE FROM N.A.
Kato H., Orito E., Gish R.G., Bzowej N., Newsom M., Sugauchi F.,
Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
"Hepatitis B e antigen in sera from individuals from patients with
hepatitis B virus of genotype G.";
Hepatology 35:922-929(2002).
EMBL; AB073445; BAB91096.1; -.
InterPro; IPR000236; TransactX.
Pfam; PF00739; X; 1.
NON TER
SEQUENCE 129 AA; 13837 MW; 2809A4B42875802E CRC64;
Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  / 1 VLHKRTLGL 9
  |||||
  67 VLHKRTLGL 75
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RX MEDLINE=21912118; PubMed=11915040;
RA Kato H., Orito E., Gish R.G., Bzowej N., Newsom M., Sugauchi F.,
RA Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
RT "Hepatitis B e antigen in sera from individuals from patients with
RT hepatitis B virus of genotype G.";
RL Hepatology 35:922-929(2002).
DR EMBL; AB073448; BAB91099.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER
SQ SEQUENCE 129 AA; 13837 MW; 2809A4B42875802E CRC64;
Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  / 1 VLHKRTLGL 9
  |||||
  67 VLHKRTLGL 75

RESULT 9
SQVT4 PRELIMINARY; PRT; 129 AA.
D Q8QVT4;
I 01-JUN-2002 (TReMBLrel. 21, Created)
I 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
I 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
E X protein (Fragment).
S X.
S Hepatitis B virus.
S Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
X NCBI_TaxID=10407;
[1]
SEQUENCE FROM N.A.
Kato H., Orito E., Gish R.G., Bzowej N., Newsom M., Sugauchi F.,
RA Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
RT "Hepatitis B e antigen in sera from individuals from patients with
RT hepatitis B virus of genotype G.";
RL Hepatology 35:922-929(2002).
DR EMBL; AB073444; BAB91095.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER
SQ SEQUENCE 129 AA; 13837 MW; 2809A4B42875802E CRC64;
Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  / 1 VLHKRTLGL 9
  |||||
  67 VLHKRTLGL 75

RESULT 10
SQVT5 PRELIMINARY; PRT; 129 AA.
D Q8QVT5;
I 01-JUN-2002 (TReMBLrel. 21, Created)
I 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
I 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
E X protein (Fragment).
S X.
S Hepatitis B virus.
S Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
X NCBI_TaxID=10407;
[1]
SEQUENCE FROM N.A.
Kato H., Orito E., Gish R.G., Bzowej N., Newsom M., Sugauchi F.,
RA Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
RT "Hepatitis B e antigen in sera from individuals from patients with
RT hepatitis B virus of genotype G.";
RL Hepatology 35:922-929(2002).
DR EMBL; AB073445; BAB91096.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER
SQ SEQUENCE 129 AA; 13837 MW; 2809A4B42875802E CRC64;
Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  / 1 VLHKRTLGL 9
  |||||
  67 VLHKRTLGL 75
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RT "Hepatitis B e antigen in sera from individuals from patients with
RT hepatitis B virus of genotype G.";
RL Hepatology 35:922-929(2002).
DR EMBL; AB073449; BAB91100.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
SQ SEQUENCE 129 AA; 13855 MW; 2809A272E87346EE CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 VLHKRTLGL 9
|||
67 VLHKRTLGL 75

RESULT 11
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AC Q8QVT7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
ON NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21912118; PubMed=11915040;
RA Kato H., Orito E., Gish R.G., Browej N., Newsom M., Sugauchi F.,
Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
RT "Hepatitis B e antigen in sera from individuals from patients with
RT hepatitis B virus of genotype G.";
RL Hepatology 35:922-929(2002).
DR EMBL; AB073441; BAB91092.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
SQ SEQUENCE 129 AA; 13836 MW; 2801063E0875802E CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
|||
67 VLHKRTLGL 75

RESULT 12
Q8QVT2 PRELIMINARY; PRT; 129 AA.
AC Q8QVT2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
ON NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21912118; PubMed=11915040;
RA Kato H., Orito E., Gish R.G., Browej N., Newsom M., Sugauchi F.,
Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
RT "Hepatitis B e antigen in sera from individuals from patients with
RT hepatitis B virus of genotype G.";
RL Hepatology 35:922-929(2002).

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 VLHKRTLGL 9
|||
67 VLHKRTLGL 75

DR EMBL; AB073446; BAB91097.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
SQ SEQUENCE 129 AA; 13837 MW; 2809A4B42875802E CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
|||
67 VLHKRTLGL 75

RESULT 13
Q8QVT6 PRELIMINARY; PRT; 129 AA.
AC Q8QVT6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
ON NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21912118; PubMed=11915040;
RA Kato H., Orito E., Gish R.G., Browej N., Newsom M., Sugauchi F.,
Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
RT "Hepatitis B e antigen in sera from individuals from patients with
RT hepatitis B virus of genotype G.";
RL Hepatology 35:922-929(2002).
DR EMBL; AB073442; BAB91093.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
SQ SEQUENCE 129 AA; 13837 MW; 2809A4B42875802E CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
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67 VLHKRTLGL 75

RESULT 14
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AC Q8QVT9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
ON NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21912118; PubMed=11915040;
RA Kato H., Orito E., Gish R.G., Browej N., Newsom M., Sugauchi F.,
Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
RT "Hepatitis B e antigen in sera from individuals from patients with
RT hepatitis B virus of genotype G.";
RL Hepatology 35:922-929(2002).
DR EMBL; AB073439; BAB91090.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.

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NON TER 1
SEQUENCE 129 AA; 13855 MW; F572172732148C1F CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VLHKRTIQL 9
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67 VLHKRTIQL 75

RESULT 15
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01-DEC-2001 (TremBrel. 19, Last sequence update)
01-MAR-2002 (TremBrel. 20, Last annotation update)
X mutant protein.
Hepatitis B virus.
Viruses; Retroviruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
[1]
SEQUENCE FROM N.A.
Dong J., Cheng J., Wang Q.;
"HEV quasispecies: X gene as an example.";
Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AF355783; AAK51832.1; -.
InterPro: IPR00236; TransactX.
Pfam: PF00739; X; 1.
SEQUENCE 130 AA; 14057 MW; 3AA3F9A206D3E31A CRC64;

Query Match 100.0%; Score 45; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VLHKRTIQL 9
|||||
92 VLHKRTIQL 100

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 Job time : 25.6 secs

GenCore version 5.1.1.6
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(without alignments)
39.666 Million cell updates/sec

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quence: 1 VLKRTLGL 9

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	45	100.0	9	4 US-09-051-006-2	Sequence 2, Appli
2	45	100.0	153	6 5196194-20	Patent No. 5196194
3	45	100.0	153	6 5204446-4	Patent No. 5204446
4	45	100.0	154	6 5183734-1	Patent No. 5183734
5	41	91.1	21	6 5183734-7	Patent No. 5183734
6	39	85.7	154	4 US-09-719-528A-5	Sequence 5, Appli
7	37	82.2	324	4 US-09-134-001C-4996	Sequence 4396, Ap
8	36	80.0	448	4 US-09-252-991A-31654	Sequence 31654, A
9	35	77.8	147	4 US-09-732-210-576	Sequence 576, App
10	34	75.6	828	4 US-09-252-991A-31556	Sequence 31556, A
11	32	71.1	250	4 US-09-252-991A-26943	Sequence 26943, A
12	32	71.1	515	4 US-09-252-991A-24984	Sequence 24984, A
13	32	71.1	599	3 US-09-357-251-14	Sequence 14, Appli
14	32	71.1	871	4 US-09-134-001C-3979	Sequence 3979, Ap
15	31	68.9	299	1 US-08-118-270-77	Sequence 77, Appli
16	31	68.9	299	5 PCT-US93-0828-77	Sequence 77, Appli
17	31	68.9	645	4 US-09-252-991A-22095	Sequence 22095, A
18	31	68.9	651	1 US-08-264-101-2	Sequence 2, Appli
19	31	68.9	651	2 US-08-765-243-2	Sequence 2, Appli
20	31	68.9	651	5 PCT-US95-07295-2	Sequence 2, Appli
21	31	68.9	734	2 US-08-765-243-8	Sequence 8, Appli
22	31	68.9	734	5 PCT-US95-07295-8	Sequence 8, Appli
23	31	68.9	1017	4 US-09-252-991A-17291	Sequence 17291, A
24	30.5	67.8	24	6 5183734-15	Patent No. 5183734
25	30	66.7	93	4 US-08-858-207A-521	Sequence 521, App
26	30	66.7	219	4 US-09-252-991A-29479	Sequence 29479, A
27	30	66.7	244	4 US-09-252-991A-23531	Sequence 23531, A

Sequence 6, Appli
Sequence 6, Appli
Sequence 11, Appli
Sequence 202, App
Sequence 202, App
Sequence 22411, A
Sequence 12, Appli
Sequence 5796, Ap
Sequence 4, Appli
Sequence 4, Appli
Sequence 31010, A
Sequence 24910, A
Sequence 28199, A
Sequence 23274, A
Sequence 4861, Ap
Sequence 4537, Ap
Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-051-006-2
; Sequence 2, Application US/09051006
; Patent No. 5380359
; GENERAL INFORMATION:
; APPLICANT: Mogam Biotechnology Research Institute
; APPLICANT: Kim, Tae-Young
; APPLICANT: Lee, Ki-Young
; APPLICANT: Chang, Jin-Soo
; APPLICANT: Cho, Sung-Yoo
; APPLICANT: Hwang, Yu-Kyeong
; APPLICANT: Choi, Myeong
; APPLICANT: Cheong, Hong-Seok
; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
; FILE OF INVENTION: Derived from X Protein of Hepatitis B virus
; FILE REFERENCE: 0136/0E154
; CURRENT APPLICATION NUMBER: US/09/051,006
; CURRENT FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-051-006-2

Query Match 100.0%; Score 45; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLKRTLGL 9

Db 1 VLKRTLGL 9

RESULT 2

5196194-20
; Patent No. 5196194
; APPLICANT: RUTTER, WILLIAM J.; GOODMAN, HOWARD M.
; TITLE OF INVENTION: VACCINES CONTAINING HEPATITIS B S-PROTEIN
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/679,621
; FILING DATE: 7-DEC-1984
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 513,055
; FILING DATE: 12-JUL-1983
; APPLICATION NUMBER: 107,267
; FILING DATE: 21-DEC-1979
; APPLICATION NUMBER: 41,909

FILING DATE: 24-MAY-1979

SEQ ID NO:20:

LENGTH: 153

196194-20

Query Match 100.0%; Score 45; DB 6; Length 153;

Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 VLHKRTLGL 9

|||||

b 92 VLHKRTLGL 100

RESULT 3

204446-4

Patent No. 5204446

APPLICANT: KIMAZAWA, TOSHIKI;OSANAI, MASATOSHI

TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY

WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS

NUMBER OF SEQUENCES: 4

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/503,239

FILING DATE: 02-APR-1990

SEQ ID NO:4:

LENGTH: 153

204446-4

Query Match 100.0%; Score 45; DB 6; Length 153;

Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 VLHKRTLGL 9

|||||

b 92 VLHKRTLGL 100

RESULT 4

5183734-1

Patent No. 5183734

APPLICANT: MORIARTY, ANN M.

TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS

FOR ASSAYING SV40 HBXAG

NUMBER OF SEQUENCES: 17

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/553,982

FILING DATE: 17-JUL-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 54,424

FILING DATE: 26-MAY-1987

APPLICATION NUMBER: 648,142

FILING DATE: 07-SEP-1984

APPLICATION NUMBER: 587,570

FILING DATE: 08-MAR-1984

SEQ ID NO:1:

LENGTH: 154

5183734-1

Query Match 100.0%; Score 45; DB 6; Length 154;

Best Local Similarity 100.0%; Pred. No. 0.051;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 VLHKRTLGL 9

|||||

b 92 VLHKRTLGL 100

RESULT 5

5183734-7

Patent No. 5183734

APPLICANT: MORIARTY, ANN M.

TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS

FOR ASSAYING SV40 HBXAG

NUMBER OF SEQUENCES: 17

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/553,982

FILING DATE: 17-JUL-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 54,424

FILING DATE: 26-MAY-1987

APPLICATION NUMBER: 648,142

FILING DATE: 07-SEP-1984

APPLICATION NUMBER: 587,570

FILING DATE: 08-MAR-1984

SEQ ID NO:7:

LENGTH: 21

5183734-7

Query Match 91.1%; Score 41; DB 6; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.044;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 VLHKRTLGL 8

|||||

b 14 VLHKRTLGL 21

RESULT 6

US-09-719-528A-5

Sequence 5, Application US/09719528A

Patent No. 6558675

GENERAL INFORMATION:

APPLICANT: Oon, Chong Jin

Lim, Gek Keow

Zhao, Yi

Chen, Wei Ning

TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND

USES THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ladas & Parry

STREET: 26 West 61 Street

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10023

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/719,528A

FILING DATE: 30-APR-2001

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/SG98/00046

FILING DATE: 19-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Mass, Clifford J.

REGISTRATION NUMBER: 30,086

REFERENCE/DOCKET NUMBER: U-013109-7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 708-1800

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 154 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-719-528A-5

Query Match 86.7%; Score 39; DB 4; Length 154;

Best Local Similarity 88.9%; Pred. No. 0.89;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 VLKRTLGL 9
||:|||||
92 VLYKRTLGL 100

SULT 7
-09-134-001C-4996
Sequence 4996 Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4996
LENGTH: 324
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
-09-134-001C-4996

Query Match 82.2%; Score 37; DB 4; Length 324;
Best Local Similarity 66.7%; Pred. No. 5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

1 VLKRTLGL 9
||:|||||
1 VLYKRTLGL 9

RESULT 8
S-09-252-991A-31654
Sequence 31654 Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31654
LENGTH: 448
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
S-09-252-991A-31654

Query Match 80.0%; Score 36; DB 4; Length 448;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 VLKRTLGL 9
||:|||||
294 VLKRTLGL 302

RESULT 9
S-09-732-210-576
Sequence 576 Application US/09732210
Patent No. 6573361
GENERAL INFORMATION:

APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Mittanck, Cindy A.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Wu, Yonnie S.

TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/09/732,210

CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 576
LENGTH: 147
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-732-210-576

Query Match 77.8%; Score 35; DB 4; Length 147;
Best Local Similarity 85.7%; Pred. No. 5.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LKRTLG 8
||:|||||
DB 84 LKRTLG 90

RESULT 10
US-09-252-991A-31556
Sequence 31556 Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31556
LENGTH: 828
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31556

Query Match 75.6%; Score 34; DB 4; Length 828;
Best Local Similarity 85.7%; Pred. No. 55;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LKRTLG 8
||:|||||
DB 740 LKRTLG 746

RESULT 11
US-09-252-991A-26943
Sequence 26943 Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26943
LENGTH: 250
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26943

Query Match 71.1%; Score 32; DB 4; Length 250;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHKRTLG 8
DB 180 LLHKREL 187

RESULT 12
US-09-252-991A-24984
Sequence 24984, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24984
LENGTH: 515
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24984

Query Match 71.1%; Score 32; DB 4; Length 515;
Best Local Similarity 55.6%; Pred. No. 88;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
DB 211 VVHRSVGL 219

RESULT 13
US-09-357-251-14
Sequence 14, Application US/09357251
Patent No. 6271441
GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Famedo, Layo O.
APPLICANT: Orozco, Buddy
APPLICANT: Schwaber, James S.
TITLE OF INVENTION: Plant Aminocacyl-tRNA Synthetase
FILE REFERENCE: BB-1193
CURRENT APPLICATION NUMBER: US/09/357,251
CURRENT FILING DATE: 1999-07-20
EARLIER APPLICATION NUMBER: 60/093,530
PRIOR FILING DATE: July 21, 1998
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 599
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: UNSURE
LOCATION: (392)..(393)..(394)

US-09-357-251-14

Query Match 71.1%; Score 32; DB 3; Length 599;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHKRTLG 8
DB 132 IMHKRTSG 139

RESULT 14
US-09-134-001C-3979
Sequence 3979, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3979
LENGTH: 871
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3979

Query Match 71.1%; Score 32; DB 4; Length 871;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHKRTLG 8
DB 571 ILHKRVVG 578

RESULT 15
US-08-118-77-77
Sequence 77, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: MURPHY=2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 77:

SEQUENCE CHARACTERISTICS:

LENGTH: 299 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

-08-118-270-77

Query Match 68.9%; Score 31; DB 1; Length 299;
Best Local Similarity 100.0%; Pred.No. 81;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VLHKRT 6

|||||

100 VLHKRT 105

Search completed: December 23, 2003, 08:53:47

Search time: 11.6 secs

GenCore version 5.1.6
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1 protein - protein search, using sw model

in on: December 23, 2003, 08:41:18 ; Search time 9.6 Seconds
(without alignments)
39.666 Million cell updates/sec

file: US-09-989-621-3

effect score: 42

sequence: 1 AMSTTDLEA 9

scoring table: BLOSUM62

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sarched: 328717 seqs, 42310858 residues

otal number of hits satisfying chosen parameters: 328717

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/2/iaa/5B COMB.pap.*

3: /cgn2_6/ptodata/2/iaa/5A COMB.pap.*

4: /cgn2_6/ptodata/2/iaa/5B COMB.pap.*

5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pap.*

6: /cgn2_6/ptodata/2/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB	ID	Description
1	42	100.0	9	4	US-09-051-006-3	Sequence 3, Appli
2	42	100.0	15	6	5183734-2	Patent No. 5183734
3	42	100.0	16	2	US-08-675-631-6	Sequence 6, Appli
4	42	100.0	16	6	5183734-16	Patent No. 5183734
5	42	100.0	17	6	5183734-8	Patent No. 5183734
6	42	100.0	153	6	5196194-20	Patent No. 5196194
7	42	100.0	153	6	5204446-4	Patent No. 5204446
8	42	100.0	154	4	US-09-719-528A-5	Sequence 5, Appli
9	42	100.0	154	6	5183734-1	Patent No. 5183734
10	38	90.5	9	3	US-08-159-339A-335	Sequence 335, App
11	38	90.5	9	4	US-09-311-784A-210	Sequence 210, App
12	33	78.6	10	3	US-08-159-339A-451	Sequence 451, App
13	33	78.6	15	3	US-08-159-339A-116	Sequence 1116, Ap
14	33	78.6	143	4	US-08-858-207A-441	Sequence 441, App
15	32	76.2	9	3	US-08-159-339A-338	Sequence 338, App
16	32	76.2	147	4	US-09-732-210-562	Sequence 562, App
17	31	73.8	469	3	US-08-985-335-5	Sequence 5, Appli
18	31	73.8	469	3	US-09-410-372-5	Sequence 5, Appli
19	31	73.8	1165	2	US-08-640-389A-11	Sequence 11, Appl
20	31	73.8	1165	2	US-08-599-455B-4	Sequence 4, Appli
21	31	73.8	1165	3	US-09-093-814-1	Sequence 1, Appli
22	31	73.8	1165	3	US-09-069-781B-4	Sequence 4, Appli
23	31	73.8	1165	3	US-08-618-957A-11	Sequence 11, Appl
24	31	73.8	1165	4	US-09-137-132-4	Sequence 4, Appli
25	31	73.8	1165	4	US-08-864-564A-4	Sequence 4, Appli
26	31	73.8	1165	4	US-09-094-410-4	Sequence 4, Appli
27	31	73.8	1165	4	US-08-708-123D-4	Sequence 4, Appli

Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 422, App
Sequence 411, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 22, Appl
Sequence 28, Appl
Sequence 3665, Ap
Sequence 16, Appl
Sequence 57, Appl
Sequence 5150, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 93, Appli

ALIGNMENTS

RESULT 1

US-09-051-006-3
; Sequence 3, Application US/09051006
; Patent No. 6380359
; GENERAL INFORMATION:
; APPLICANT: Mogan Biotechnology Research Institute
; APPLICANT: Kim, Tae-Young
; APPLICANT: Lee, Ki-Young
; APPLICANT: Chang, Jin-Soo
; APPLICANT: Cho, Sung-Yoo
; APPLICANT: Hwang, Yu-Kyeong
; APPLICANT: Choi, Myeong
; APPLICANT: Cheong, Hong-Seok
; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
; FILE REFERENCE: 0136/OE154
; CURRENT APPLICATION NUMBER: US/09/051,006
; CURRENT FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-051-006-3

Query Match 100.0%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9

Db 1 AMSTTDLEA 9

RESULT 2

5183734-2
; Patent No. 5183734
; APPLICANT: MORIARTY, ANN M.
; TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
; FOR ASSAYING SV40 HBXAG
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,982
; FILING DATE: 17-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 54,424
; FILING DATE: 26-MAY-1987
; APPLICATION NUMBER: 648,142
; FILING DATE: 07-SEP-1984

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RESULT 4
5183734-16
;Patent No. 5183734
; APPLICANT: MORIARTY, ANN M.
; TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
; FOR ASSAYING SV40 HEXAG
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,982
; FILING DATE: 17-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 54,424
; FILING DATE: 26-MAY-1987
; APPLICATION NUMBER: 648,142
; FILING DATE: 07-SEP-1984
; APPLICATION NUMBER: 587,570
; FILING DATE: 08-MAR-1984
; SEQ ID NO:16:
; LENGTH: 16
5183734-16
Query Match 100.0%; Score 42; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 3 AMSTTDLEA 11

RESULT 5
5183734-8
;Patent No. 5183734
; APPLICANT: MORIARTY, ANN M.
; TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
; FOR ASSAYING SV40 HEXAG
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,982
; FILING DATE: 17-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 54,424
; FILING DATE: 26-MAY-1987
; APPLICATION NUMBER: 648,142
; FILING DATE: 07-SEP-1984
; APPLICATION NUMBER: 587,570
; FILING DATE: 08-MAR-1984
; SEQ ID NO:8:
; LENGTH: 17
5183734-8
Query Match 100.0%; Score 42; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 4 AMSTTDLEA 12

RESULT 6
5196194-20
;Patent No. 5196194
; APPLICANT: RUTTER, WILLIAM J.;GOODMAN, HOWARD M.
; TITLE OF INVENTION: VACCINES CONTAINING HEPATITIS B S-PROTEIN
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/679,621
; FILING DATE: 7-DEC-1984
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 513,055

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FILING DATE: 12-JUL-1983
 APPLICATION NUMBER: 107,267
 FILING DATE: 21-DEC-1979
 APPLICATION NUMBER: 41,909
 FILING DATE: 24-MAY-1979
 EQ ID NO: 20
 LENGTH: 153
 96194-20

Query Match 100.0%; Score 42; DB 6; Length 153;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AMSTTDLEA 9
 |||||
 102 AMSTTDLEA 110

RESULT 7
 Patent No. 5204446
 APPLICANT: KUNAZAWA, TOSHIKAKI, OSANAI, MASATOSHI
 TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY
 WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS
 NUMBER OF SEQUENCES: 4
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/503,239
 FILING DATE: 02-APR-1990
 EQ ID NO: 4;
 LENGTH: 153
 204446-4

Query Match 100.0%; Score 42; DB 6; Length 153;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AMSTTDLEA 9
 |||||
 102 AMSTTDLEA 110

RESULT 8
 3-09-719-528A-5
 Sequence 5, Application US/09719528A
 Patent No. 6558675
 GENERAL INFORMATION:
 APPLICANT: Oon, Chong Jin
 Lim, Gek Keow
 Zhao, Yi
 Chen, Wei Ning

TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
 USES THEREOF

NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ladas & Parry
 STREET: 26 West 61 Street
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10023

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/719,528A
 FILING DATE: 30-Apr-2001
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/SG98/00046
 FILING DATE: 19-JAN-1998
 ATTORNEY/AGENT INFORMATION:

NAME: Mass, Clifford J.
 REGISTRATION NUMBER: 30,086
 REFERENCE/DOCKET NUMBER: U-013109-7
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 708-1800
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 154 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-09-719-528A-5

Query Match 100.0%; Score 42; DB 4; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 |||||
 DB 102 AMSTTDLEA 110

RESULT 9
 5183734-1
 Patent No. 5183734
 APPLICANT: MORIARTY, ANN M.
 TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
 FOR ASSAYING SV40 HEXAG
 NUMBER OF SEQUENCES: 17
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/553,982
 FILING DATE: 17-JUL-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 54,424
 FILING DATE: 26-MAY-1987
 APPLICATION NUMBER: 648,142
 FILING DATE: 07-SEP-1984
 APPLICATION NUMBER: 587,570
 FILING DATE: 08-MAR-1984
 EQ ID NO: 1;
 LENGTH: 154
 5183734-1

Query Match 100.0%; Score 42; DB 6; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 |||||
 DB 102 AMSTTDLEA 110

RESULT 10
 US-08-159-339A-335
 Sequence 335, Application US/08159339A
 Patent No. 6037135
 GENERAL INFORMATION:
 APPLICANT: Kubo, Ralph T.
 APPLICANT: Grey, Howard M.
 APPLICANT: Sette, Alessandro
 APPLICANT: Celis, Esteban
 TITLE OF INVENTION: HLA Binding peptides and Their
 TITLE OF INVENTION: Uses
 NUMBER OF SEQUENCES: 1254
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993

ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
TELEX:

INFORMATION FOR SEQ ID NO: 335:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
S-08-159-339A-335

Query Match 90.5%; Score 38; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 MSTDLEA 9
1 MSTDLEA 8

RESULT 11
US-09-311-784A-210
Sequence 210, Application US/09311784A
Patent No. 6534482

GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.

APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.

APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
TITLE OF INVENTION: Immune Response and Methods of Using the Same

FILE REFERENCE: 39963-20022.01
CURRENT APPLICATION NUMBER: US/09/311,784A
CURRENT FILING DATE: 1999-05-13

PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 210
LENGTH: 9
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HBV adr 1521 (peptide 2.0126)

US-09-311-784A-210
Query Match 90.5%; Score 38; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTDLEA 9
Db 1 MSTDLEA 8

RESULT 12

US-08-159-339A-451
Sequence 451, Application US/08159339A
Patent No. 6037135

GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.

APPLICANT: Sette, Alessandro
APPLICANT: Celis, Eteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses

NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco

STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993

APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 451:
SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-159-339A-451
Query Match 78.8%; Score 33; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MSTDLEA 9
Db 1 MSTDLEA 7

RESULT 13

US-08-159-339A-1116
Sequence 1116, Application US/08159339A
Patent No. 6037135

GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.

APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993

ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:

INFORMATION FOR SEQ ID NO: 1116:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

3-08-159-339A-1116

Query Match 78.6%; Score 33; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3 STTDLEA 9

1 STTDLEA 7

RESULT 14

3-08-858-207A-441
Sequence 441, Application US/08858207A
Patent No. 6348328

GENERAL INFORMATION:

APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328a1 Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA

ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R

REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:

INFORMATION FOR SEQ ID NO: 441:

SEQUENCE CHARACTERISTICS:
LENGTH: 143 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6348328e

US-08-858-207A-441

Query Match 78.6%; Score 33; DB 4; Length 143;
Best Local Similarity 77.8%; Pred. No. 9.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9

DB 93 ALSTPDLEA 101

RESULT 15

US-08-159-339A-338
Sequence 338, Application US/08159339A
Patent No. 6037135

GENERAL INFORMATION:

APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/159,339A

FILING DATE: 29-NOV-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/926,666

FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 08/027,746

FILING DATE: 05-MAR-1993

APPLICATION NUMBER: US 08/103,396

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; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-0050300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 338:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-338

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Query Match 76.2%; Score 32; DB 3; Length 9;
Best Local Similarity 97.5%; Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY / 2 MSTTDLEA 9
Db 1 MSPTDLEA 8

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Search completed: December 23, 2003, 08:53:49
Job time : 11.6 secs

GenCore version 5.1.6
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M protein - protein search, using sw model

un on: December 23, 2003, 08:40:03 ; Search time 79.4 Seconds
(without alignments)
21.169 Million cell updates/sec

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effect score: 42
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Gapop 10.0 , Gapext 0.5

earched: 696363 seqs, 186758610 residues

otal number of hits satisfying chosen parameters: 696363

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	42	100.0	9	US-09-989-621-3
2	42	100.0	154	US-10-209-264-5
3	38	90.5	9	US-10-371-069-210
4	38	90.5	9	US-10-371-645-210
5	38	90.5	9	US-10-371-260-210
6	32	76.2	525	US-09-881-752A-96
7	31	73.8	133	US-10-038-010-42
8	31	73.8	308	US-10-038-010-46
9	31	73.8	346	US-09-925-301-1211
10	31	73.8	469	US-09-894-657-5
11	31	73.8	1165	US-08-779-457-2
12	31	73.8	1165	US-10-079-625-4
13	31	73.8	1165	US-10-095-929-11
14	31	73.8	1165	US-10-214-802-2
15	31	73.8	1165	US-10-226-579-4

16	30	71.4	109	12	US-10-094-749-2129	Sequence 2129, Ap
17	29	69.0	208	15	US-10-156-761-8314	Sequence 8314, Ap
18	29	69.0	212	15	US-10-156-761-7969	Sequence 7969, Ap
19	29	69.0	640	14	US-10-047-676A-16	Sequence 16, Appl
20	29	69.0	965	12	US-10-262-794A-57	Sequence 57, Appl
21	29	69.0	965	15	US-10-242-056-57	Sequence 57, Appl
22	29	69.0	1726	12	US-10-205-219-109	Sequence 109, Appl
23	29	69.0	4695	15	US-10-156-761-10433	Sequence 10433, A
24	28	66.7	69	15	US-10-062-548-93	Sequence 93, Appl
25	28	66.7	75	11	US-09-764-891-4099	Sequence 4099, Ap
26	28	66.7	114	9	US-09-925-299-976	Sequence 976, App
27	28	66.7	114	11	US-09-925-299-976	Sequence 976, App
28	28	66.7	222	11	US-09-738-626-4748	Sequence 4748, Ap
29	28	66.7	287	10	US-09-738-626-5719	Sequence 5719, Ap
30	28	66.7	310	15	US-10-146-772-32	Sequence 32, Appl
31	28	66.7	317	10	US-09-738-626-6917	Sequence 6917, Ap
32	28	66.7	321	12	US-10-032-201B-222	Sequence 222, App
33	28	66.7	322	10	US-09-990-415A-8	Sequence 8, Appli
34	28	66.7	322	15	US-10-014-338-2	Sequence 2, Appli
35	28	66.7	326	10	US-09-738-626-4959	Sequence 4959, Ap
36	28	66.7	335	12	US-10-032-201B-217	Sequence 217, App
37	28	66.7	338	10	US-09-738-626-6332	Sequence 6332, Ap
38	28	66.7	355	10	US-09-951-769-2	Sequence 2, Appli
39	28	66.7	532	12	US-10-032-585-7043	Sequence 7043, Ap
40	28	66.7	755	9	US-09-881-852-19	Sequence 19, Appl
41	28	66.7	1274	12	US-10-032-585-7010	Sequence 7010, Ap
42	28	66.7	1591	12	US-10-238-075-947	Sequence 947, App
43	27	64.3	90	10	US-09-976-059-12	Sequence 12, Appl
44	27	64.3	159	12	US-10-353-174-4	Sequence 4, Appli
45	27	64.3	160	15	US-10-156-761-10933	Sequence 10933, A

ALIGNMENTS

RESULT 1

US-09-989-621-3
; Sequence 3, Application US/09989621
; Patent No. US20020151683A1
; GENERAL INFORMATION:
; APPLICANT: Mogam Biotechnology Research Institute
; APPLICANT: Kim, Tae-Young
; APPLICANT: Lee, Ki-Young
; APPLICANT: Chang, Jin-Soo
; APPLICANT: Cho, Sung-Yoo
; APPLICANT: Hwang, Yu-Kyeong
; APPLICANT: Choi, Myeong
; APPLICANT: Cheong, Hong-Seok
; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
; FILE OF INVENTION: Derived from X Protein of Hepatitis B virus
; FILE REFERENCE: 0136/0E154
; CURRENT APPLICATION NUMBER: US/09/989,621
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/051,006
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-989-621-3

Query Match 100.0%; Score 42; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMSTTDLEA 9

DB 1 AMSTTDLEA 9

RESULT 2

US-10-209-264-5
 ; Sequence 5, Application US/10209264
 ; Publication No. US20030003111A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Oon, Chong Jin
 ; Lim, Gek Keow
 ; Zhao, Yi
 ; Chen, Wei Ning
 ; TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
 ; USES THEREOF
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ladas & Parry
 ; STREET: 26 West 61 Street
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10023
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/209,264
 ; FILING DATE: 31-Jul-2002
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/SG98/00046
 ; FILING DATE: 19-JAN-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mass, Clifford J.
 ; REGISTRATION NUMBER: 30,086
 ; REFERENCE/DOCKET NUMBER: U-013109-7
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 708-1800
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 154 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-10-209-264-5
 Query Match 100.0%; Score 42; DB 15; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.37; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;
 QY 1 AMSTTDLEA 9
 DB 102 AMSTTDLEA 110
 RESULT 3
 US-10-371-069-210
 ; Sequence 210, Application US/10371069
 ; Publication No. US20030216342A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EPIMMUNE Inc.
 ; APPLICANT: Fikes, John D.
 ; APPLICANT: Hermanson, Gary G.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Ishioka, Glenn Y.
 ; APPLICANT: Livingston, Brian
 ; APPLICANT: Chesnut, Robert W.
 ; APPLICANT: Epimmune Inc.
 ; TITLE OF INVENTION: Expression Vectors for Stimulating an
 ; FILE OF INVENTION: Immune Response and Methods of Using the Same
 ; FILE REFERENCE: 39963-20022.10
 ; CURRENT APPLICATION NUMBER: US/10/371,069
 ; PRIOR FILING DATE: 2003-02-21
 ; CURRENT FILING DATE: 2003-02-21
 ; PRIOR APPLICATION NUMBER: US/09/078,904

; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: US 60/085,751
 ; PRIOR FILING DATE: 1998-05-15
 ; NUMBER OF SEQ ID NOS: 463
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 210
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: HBV adr 1521 (peptide 2.0126)
 US-10-371-069-210
 Query Match 90.5%; Score 38; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.2e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MSTTDLEA 9
 DB 1 MSTTDLEA 8
 RESULT 4
 US-10-371-645-210
 ; Sequence 210, Application US/10371645
 ; Publication No. US20030216343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EPIMMUNE Inc.
 ; APPLICANT: Fikes, John D.
 ; APPLICANT: Hermanson, Gary G.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Ishioka, Glenn Y.
 ; APPLICANT: Livingston, Brian
 ; APPLICANT: Chesnut, Robert W.
 ; APPLICANT: Epimmune Inc.
 ; TITLE OF INVENTION: Expression Vectors for Stimulating an
 ; FILE OF INVENTION: Immune Response and Methods of Using the Same
 ; FILE REFERENCE: 39963-20022.11
 ; CURRENT APPLICATION NUMBER: US/10/371,645
 ; PRIOR FILING DATE: 2003-06-20
 ; PRIOR APPLICATION NUMBER: US 09/078,904
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: US 60/085,751
 ; PRIOR FILING DATE: 1998-05-15
 ; NUMBER OF SEQ ID NOS: 463
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 210
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: HBV adr 1521 (peptide 2.0126)
 US-10-371-645-210
 Query Match 90.5%; Score 38; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.2e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MSTTDLEA 9
 DB 1 MSTTDLEA 8
 RESULT 5
 US-10-371-260-210
 ; Sequence 210, Application US/10371260
 ; Publication No. US20030220285A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EPIMMUNE Inc.
 ; APPLICANT: Fikes, John D.
 ; APPLICANT: Hermanson, Gary G.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Ishioka, Glenn Y.

; APPLICANT: Livingston, Brian
 ; APPLICANT: Chesnut, Robert W.
 ; APPLICANT: Epiimmune Inc.
 ; TITLE OF INVENTION: Expression Vectors for Stimulating an
 ; FILE REFERENCE: 39963-20022.13
 ; CURRENT APPLICATION NUMBER: US/10/371,260
 ; PRIOR FILING DATE: 2003-02-21
 ; PRIOR APPLICATION NUMBER: US 09/078,904
 ; PRIOR FILING DATE: 1998-03-13
 ; PRIOR APPLICATION NUMBER: US 60/085,751
 ; PRIOR FILING DATE: 1998-05-15
 ; NUMBER OF SEQ ID NOS: 463
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 210
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: HBV adr 1521 (peptide 2.0126)
 ; S-10-371-260-210

Query Match 90.5%; Score 38; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.2e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 MSTTDLEA 9
 |||||
 b 1 MSTTDLEA 8
 |||||

RESULT 6
 S-09-881-752A-96
 ; Sequence 96, Application US/09881752A
 ; Patent No. US20020115078A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kleanthous, Harold
 ; APPLICANT: Al-Garawi, Amal
 ; APPLICANT: Miller, Charles
 ; APPLICANT: Tomb, Jean-Francois
 ; APPLICANT: Oomen, Raymond P.
 ; TITLE OF INVENTION: Identification of Polynucleotides
 ; FILE REFERENCE: Encoding No. US20020115078A1 Helicobacter Polypeptides in the
 ; TITLE OF INVENTION: Genome
 ; FILE REFERENCE: 06132/041002
 ; CURRENT APPLICATION NUMBER: US/09/881,752A
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: US 08/833,457
 ; PRIOR FILING DATE: 1997-04-01
 ; NUMBER OF SEQ ID NOS: 370
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 96
 ; LENGTH: 525
 ; TYPE: PRT
 ; ORGANISM: Helicobacter pylori
 ; S-09-881-752A-96

Query Match 76.2%; Score 32; DB 10; Length 525;
 Best Local Similarity 77.8%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1 AMSTTDLEA 9
 |||||
 b 208 AMKWTDLA 216
 |||||

RESULT 7
 S-10-038-010-42
 ; Sequence 42, Application US/10038010
 ; Publication No. US20030040089A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HYBRIGENICS
 ; APPLICANT: Pierre, Legrain

; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
 ; FILE REFERENCE: B4767A
 ; CURRENT APPLICATION NUMBER: US/10/038,010
 ; CURRENT FILING DATE: 2002-07-23
 ; PRIOR APPLICATION NUMBER: US 60/259,377
 ; PRIOR FILING DATE: 2001-01-02
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 42
 ; LENGTH: 133
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: hOB-receptor long form
 ; LOCATION: (1)..(133)
 ; OTHER INFORMATION:
 ; US-10-038-010-42

Query Match 73.8%; Score 31; DB 15; Length 133;
 Best Local Similarity 85.7%; Pred. No. 62;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MSTTDLE 8
 :|||||
 Db 86 LSTTDLE 92

RESULT 8
 US-10-038-010-46
 ; Sequence 46, Application US/10038010
 ; Publication No. US20030040089A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HYBRIGENICS
 ; APPLICANT: Pierre, Legrain
 ; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
 ; FILE REFERENCE: B4767A
 ; CURRENT APPLICATION NUMBER: US/10/038,010
 ; CURRENT FILING DATE: 2002-07-23
 ; PRIOR APPLICATION NUMBER: US 60/259,377
 ; PRIOR FILING DATE: 2001-01-02
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 46
 ; LENGTH: 308
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: hOB-receptor long form
 ; LOCATION: (1)..(308)
 ; OTHER INFORMATION:
 ; US-10-038-010-46

Query Match 73.8%; Score 31; DB 15; Length 308;
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MSTTDLE 8
 :|||||
 Db 86 LSTTDLE 92

RESULT 9
 US-09-925-301-1211
 ; Sequence 1211, Application US/09925301
 ; Patent No. US20020052308A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PAL06
 ; CURRENT APPLICATION NUMBER: US/09/925,301
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05982
 ; PRIOR FILING DATE: 2000-03-08

;; PRIOR APPLICATION NUMBER: 60/124,270
;; PRIOR FILING DATE: 1999-03-12
;; NUMBER OF SEQ ID NOS: 1694
;; SOFTWARE: Patent in Ver. 2.0
;; SEQ ID NO 1211
;; LENGTH: 346
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-925-301-1211

Query Match 73.8%; Score 31; DB 9; Length 346;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MSTDLE 8
Db 108 MSTDLE 114

RESULT 10
US-09-894-657-5
; Sequence 5, Application US/09894657
; Patent No. US20020098569A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Inve, Henry
; Lal, Preeti
; Shah, Purvi
; Corley, Neil C.

TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
PROLIFERATION

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/894,657

FILING DATE: 28-Jun-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/410,372

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0421 US

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 469 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: QVARTUT01

CLONE: 815087

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-894-657-5

Query Match 73.8%; Score 31; DB 9; Length 469;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MSTDLE 8
Db 231 MSTDLE 237

RESULT 11
US-08-779-457-2
; Sequence 2, Application US/08779457
; Publication No. US20020193571A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.

APPLICANT: Chiang, Nancy Y.

APPLICANT: Kyung, Jin Kim

APPLICANT: Matthews, William

APPLICANT: Rodrigues, Maria L.

TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Pointe San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/779,457

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/667197

FILING DATE: 06/20/96

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/585005

FILING DATE: 01/08/96

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P0986P2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1994

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1165 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-779-457-2

Query Match 73.8%; Score 31; DB 8; Length 1165;
Best Local Similarity 85.7%; Pred. No. 6.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MSTDLE 8
Db 943 LSTDLE 949

RESULT 12
US-10-079-625-4
; Sequence 4, Application US/10079625
; Publication No. US20020182676A1
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.

APPLICANT: Tepper, Robert I.

APPLICANT: Cupepper, Janice A.

APPLICANT: White, David W.

TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR

TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
INCLUDING OBESITY AND CACHEXIA

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/079,625

FILING DATE: 2002-FEB-19

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/864,564

FILING DATE: 28-MAY-1997

APPLICATION NUMBER: 08/708,123

FILING DATE: 03-SEP-1996

APPLICATION NUMBER: 08/638,524

FILING DATE: 26-APR-1996

APPLICATION NUMBER: 08/599,455

FILING DATE: 22-JAN-1996

APPLICATION NUMBER: 08/583,153

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: 08/570,142

FILING DATE: 11-DEC-1995

APPLICATION NUMBER: 08/569,485

FILING DATE: 08-DEC-1995

APPLICATION NUMBER: 08/566,622

FILING DATE: 04-DEC-1995

APPLICATION NUMBER: 08/562,663

FILING DATE: 27-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: Meiklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/019002

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1165 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

S-10-079-625-4

Query Match

Best Local Similarity 73.8%; Score 31; DB 14; Length 1165;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 2 MSTTDL 8

:|||||

b 943 LSTTDL 949

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/214,802

FILING DATE: 06-AUG-2002

RESULT 13

S-10-095-929-11

Sequence 11, Application US/10095929

Publication No. US2002019732A1

GENERAL INFORMATION:

APPLICANT: Snodgrass, H. Ralph

Cioffi, Joseph

Zupancic, Thomas Joel

Shater, Alan Wayne

TITLE OF INVENTION: METHODS FOR USING THE OBSE

GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
DEVELOPMENT

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of The Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/095,929

FILING DATE: 12-Mar-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/618,957

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Poissant, Brian M.

REGISTRATION NUMBER: 28,462

REFERENCE/DOCKET NUMBER: 008907-0033-999

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 1165 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-10-095-929-11

Query Match

Best Local Similarity 73.8%; Score 31; DB 14; Length 1165;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 2 MSTTDL 8

:|||||

Db 943 LSTTDL 949

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/214,802

FILING DATE: 06-AUG-2002

RESULT 14

US-10-214-802-2

Sequence 2, Application US/10214802

Publication No. US20030004109A1

GENERAL INFORMATION:

APPLICANT: Matthews, William

Bennett, Brian

TITLE OF INVENTION: WSX RECEPTOR

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/214,802

FILING DATE: 06-AUG-2002

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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,562
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/585005
; FILING DATE: 08-Jan-97
; APPLICATION NUMBER: 60/
; FILING DATE: 08-Jan-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P098631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1394
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-214-802-2
Query Match 73.8%; Score 31; DB 15; Length 1165;
Best Local Similarity 85.7%; Pred. NO. 6.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTTDL 8
DB 943 LSTTDL 949

RESULT 15
US-10-226-579-4
; Sequence 4, Application US/10226579
; Publication No. US20030073634A1
; GENERAL INFORMATION:
; APPLICANT: Myers, Martin
; TITLE OF INVENTION: METHODS OF TREATING OBESITY
; FILE REFERENCE: 10276-071001
; CURRENT APPLICATION NUMBER: US/10/226,579
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: US 60/314,976
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-226-579-4
Query Match 73.8%; Score 31; DB 15; Length 1165;
Best Local Similarity 85.7%; Pred. NO. 6.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTTDL 8
DB 943 LSTTDL 949

Search completed: December 23, 2003, 08:52:49
Job time : 80.4 secs
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GenCore version 5.1.6
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*M protein - protein search, using sw model

run on: December 23, 2003, 08:39:57 ; Search time 11 Seconds
(without alignments)
78.683 Million cell updates/sec

itle: US-09-989-621-3

erfect score: 42

equence: 1 AMSTTDLEA 9

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

earched: 283308 seqs, 96168682 residues

otal number of hits satisfying chosen parameters: 283308

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

PIR 76:**

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	42	100.0	134	1 B48345	Gene X protein, tr
2	42	100.0	154	1 QQVLDI	Gene X protein - h
3	42	100.0	154	1 A48345	Gene X protein - h
4	42	100.0	154	1 QQVLAH	Gene X protein - h
5	42	100.0	154	1 QQVLAH	Gene X protein - h
6	42	100.0	154	1 QQVLAH	Gene X protein - h
7	42	100.0	154	2 S20756	Gene X protein - h
8	42	100.0	154	2 S47408	Gene X protein - h
9	42	100.0	154	2 S20256	Gene X protein - h
10	42	100.0	154	2 S25650	Gene X protein - h
11	42	100.0	154	2 S53130	Gene X protein - h
12	42	100.0	154	2 JS0603	Gene X protein - h
13	42	100.0	154	2 JS0604	Gene X protein - h
14	42	100.0	154	2 S35529	Gene X protein - h
15	42	100.0	154	2 S33687	Gene X protein - h
16	42	100.0	154	2 S12542	Gene X protein - h
17	42	100.0	154	2 S32203	Gene X protein - h
18	42	100.0	154	2 S22319	Gene X protein - h
19	42	100.0	154	2 S20751	Gene X protein - h
20	42	100.0	154	2 T13466	Gene X protein - h
21	42	100.0	172	2 A58456	Gene X protein - h
22	42	100.0	210	2 T13472	X protein - human
23	38	90.5	154	2 S12598	Gene X protein - h
24	38	90.5	154	1 QQVLAH	Gene X protein - h
25	38	90.5	154	1 QQVLAH	Gene X protein - h
26	38	90.5	359	2 S04570	Gene X protein - h
27	35	83.3	203	2 S50728	Gene X/C fusion pr
28	35	83.3	506	2 AG0693	probable membrane
29	33	78.6	126	2 B95111	aerotoxis receptor

30 78.6 131 2 AB1525 hypothetical prote
31 78.6 143 2 H97979 lactoylglutathione
32 78.6 191 2 S29008 ADP-ribosylation f
33 78.6 526 2 D71805 protein-export mem
34 76.2 56 2 AB2565 hypothetical prote
35 76.2 147 2 S66576 ribosomal protein
36 76.2 154 2 E87029 hypothetical prote
37 76.2 164 2 S28525 hypothetical prote
38 76.2 503 1 F64713 protein-export mem
39 76.2 506 2 E65095 aerotoxis receptor
40 76.2 506 2 A85968 aerotoxis sensor r
41 76.2 506 2 B91123 aerotoxis sensor r
42 73.8 402 2 S47329 OXAL protein precu
43 73.8 458 2 JC5193 nuclear protein H7
44 73.8 465 2 S40701 hypothetical prote
45 73.8 506 2 B84339 hypothetical prote

ALIGNMENTS

RESULT 1

B48345
Gene X protein, truncated form - hepatitis B virus

C:Species: hepatitis B virus, HBV

C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999

C:Accession: B48345

R:Repp. R.; Keller, C.; Borkhardt, A.; Csecke, A.; Schaefer, S.; Gerlich, W.H.; Lampert, Arch. Virol. 125, 299-304, 1992

A:Title: Detection of a hepatitis B virus variant with a truncated X gene and enhancer I

A:Reference number: A48345; MUID:92352333; PMID:1642555

A:Accession: B48345

A:Molecule type: DNA

A:Residues: 1-134 <REP>

A:Cross-references: GB:S41176; NID:G252541; PIDN:AB22733.1; PID:G252542

A:Note: sequence extracted from NCBI backbone (NCBIN:109914; NCBI:P:109915)

C:Genetics:

A:Gene: X

C:Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 42; DB 1; Length 134;

Best Local Similarity 100.0%; Pred. NO. 0.065;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9

DB 102 AMSTTDLEA 110

RESULT 2

QQVLDI

Gene X protein - hepatitis B virus (subtype ayw)

C:Species: hepatitis B virus, HBV

C:Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 08-Apr-1994

C:Accession: A03719

R:Calibert, F.; Mandart, E.; Fitoussi, P.; Tiollais, P.; Charnay, P.

Nature 281, 646-650, 1979

A:Title: Nucleotide sequence of the hepatitis B virus genome (subtype ayw) in E. coli.

A:Reference number: A93214; MUID:81012091; PMID:399327

A:Accession: A03719

A:Molecule type: DNA

A:Residues: 1-154 <GAL>

A:Cross-references: GB:J02203; GB:V01460

C:Genetics:

A:Gene: X

C:Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 42; DB 1; Length 154;

Best Local Similarity 100.0%; Pred. NO. 0.075;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9

|||||

```

Db      102 AMSTTDLEA 110

RESULT 3
A48345
Gene X protein - hepatitis B virus
C:Species: hepatitis B virus, HBV
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C:Accession: A48345
R:Repp, R.; Keller, C.; Borkhardt, A.; Csecke, A.; Schaefer, S.; Gerlich, W.H.; Lampert,
Arch. Virol. 125, 299-304, 1992
A:Title: Detection of a hepatitis B virus variant with a truncated X gene and enhancer II
A:Reference number: A48345; MUID:92352333; PMID:1642555
A:Accession: A48345
A:Molecule type: DNA
A:Residues: 1-154 <REP>
A:Cross-references: GB:S41175; NID:g252539; PIDN:AB22732.1; PID:g252540
A>Note: sequence extracted from NCBI backbone (NCBI:109912, NCSIP:109913)
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 42; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AMSTTDLEA 9
      |||||||
Db      102 AMSTTDLEA 110

RESULT 4
QQVLAW
Gene X protein - hepatitis B virus (subtype adw and adw2)
C:Species: hepatitis B virus, HBV
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 30-Jun-1998
C:Accession: A31289; B94409; A03719
R:Lo, S.J.; Chien, M.L.; Lee, Y.H.W.
Virology 167, 289-292, 1988
A:Title: Characteristics of the X gene of hepatitis B virus.
A:Reference number: A31289; MUID:89045656; PMID:3188399
A:Accession: A31289
A:Molecule type: DNA
A:Residues: 1-154 <LOS>
A:Experimental source: subtype adw
R:Valenzuela, P.; Quiroga, M.; Zaldivar, J.; Gray, P.; Rutter, W.J.
in Animal Virus Genetics, Field, B.N., Jaenisch, R., and Fox, C.F., eds., pp.57-70, Academic Press, 1989
A:Reference number: A94409
A:Accession: B94409
A:Molecule type: DNA
A:Residues: 1-154 <VAL>
A:Experimental source: subtype adw2
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 42; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AMSTTDLEA 9
      |||||||
Db      102 AMSTTDLEA 110

RESULT 5
QQVLKS
Gene X protein - hepatitis B virus (subtype adw, strain 991)
C:Species: hepatitis B virus, HBV
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: A10380
R:Koechel, H.G.; Schueler, A.; Lottmann, S.; Thomssen, R.
submitted to the EMBL Data Library, February 1990

```

```

A:Reference number: S10380
A:Accession: S10380
A:Molecule type: DNA
A:Residues: 1-154 <KOE>
A:Cross-references: EMBL:X51970; NID:g1155012; PIDN:CAA36231.1; PID:g60432
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 42; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AMSTTDLEA 9
      |||||||
Db      102 AMSTTDLEA 110

RESULT 6
S20756
Gene X protein - hepatitis B virus (subtype ayw, patient E)
C:Species: hepatitis B virus, HBV
A:Variety: subtype ayw, patient E
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S20756
R:Lai, M.B.; Mazzoleni, A.P.; Balestrieri, A.; Mellis, A.; Porru, A.
submitted to the EMBL Data Library, March 1992
A:Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negative
A:Reference number: S20745
A:Accession: S20756
A:Molecule type: DNA
A:Residues: 1-154 <LAI>
A:Cross-references: EMBL:X65259; NID:g59439; PIDN:CAA46360.1; PID:g59443
A:Experimental source: subtype ayw, patient E
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 42; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AMSTTDLEA 9
      |||||||
Db      102 AMSTTDLEA 110

RESULT 7
S47408
Gene X protein - hepatitis B virus (subtype adw2)
C:Species: hepatitis B virus, HBV
A:Variety: subtype adw2
C:Date: 23-Nov-1994 #sequence_revision 12-May-1995 #text_change 26-Aug-1999
C:Accession: S47408
R:Plucieniczak, A.
submitted to the EMBL Data Library, August 1994
A:Description: Molecular cloning and sequencing of two complete genomes of polish isolates
A:Reference number: S47404
A:Accession: S47408
A:Molecule type: DNA
A:Residues: 1-154 <PLU>
A:Cross-references: EMBL:Z35717; NID:g527440; PIDN:CAA84789.1; PID:g527441
A:Experimental source: subtype adw2
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 42; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AMSTTDLEA 9
      |||||||

```

```
b 102 AMSTTDLEA 110

RESULT 8
S0256
ene X protein - hepatitis B virus (subtype adw, strain Japan/PJDW233)
;Species: hepatitis B virus, HBV
;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 14-Nov-1997
;Accession: J0256
;Okamoto, H.; Tsuda, F.; Sakugawa, H.; Sastrosoewignjo, R.I.; Imai, M.; Miyakawa, Y.; M
. Gen. Virol. 69, 2575-2583, 1988
;Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of surfa
;Reference number: J0253; MUID:89010694; PMID:3171552
;Accession: J0256
;Status: translation not shown
;Molecule type: DNA
;Residues: 1-154 <OKA>
;Cross-references: GB:D00329; NID:g221497
;Genetics:
;Gene: X
;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 42; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 AMSTTDLEA 9
|||||
b 102 AMSTTDLEA 110

RESULT 9
25650
ene X protein - hepatitis B virus (subtype ayw, patient D)
;Species: hepatitis B virus, HBV
;Variety: subtype ayw, patient D
;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
;Accession: S25650
;Lai, M.E.; Mazzoleni, A.P.; Melis, A.; Balestrieri, A.
ubmitted to the EMBL Data Library, September 1992
;Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negati
;Reference number: S25650
;Accession: S25650
;Molecule type: DNA
;Residues: 1-154 <LAI>
;Cross-references: EMBL:X68292; NID:G59448; PIDN:CAA48352.1; PID:G59449
;Experimental source: subtype ayw, patient D
;Genetics:
;Gene: X
;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 42; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

f 1 AMSTTDLEA 9
|||||
c 102 AMSTTDLEA 110

RESULT 10
53130
ene X protein - hepatitis B virus
;Species: hepatitis B virus, HBV
;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
;Accession: S53130
;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
ubmitted to the EMBL Data Library, March 1995
;Reference number: S53112
;Accession: S53130
;Molecule type: DNA
;Residues: 1-154 <LAI>
;Cross-references: EMBL:X85254; NID:g736003; PIDN:CAA59513.1; PID:g736007

C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 42; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
|||||
DB 102 AMSTTDLEA 110

RESULT 11
J0603
ene X protein - hepatitis B virus (subtype adw, strain Okinawa/P0DW282)
;Species: hepatitis B virus, HBV
;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 14-Nov-1997
;Accession: J0603
;Okamoto, H.; Tsuda, F.; Sakugawa, H.; Sastrosoewignjo, R.I.; Imai, M.; Miyakawa, Y.; M
. Gen. Virol. 69, 2575-2583, 1988
;Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of surfa
;Reference number: J0253; MUID:89010694; PMID:3171552
;Accession: J0603
;Status: translation not shown
;Molecule type: DNA
;Residues: 1-154 <OKA>
;Cross-references: GB:D00330; NID:g221498
;Genetics:
;Gene: X
;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 42; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
|||||
DB 102 AMSTTDLEA 110

RESULT 12
J0604
ene X protein - hepatitis B virus (subtype adw, strain Indonesia/PIDW420)
;Species: hepatitis B virus, HBV
;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 14-Nov-1997
;Accession: J0604
;Okamoto, H.; Tsuda, F.; Sakugawa, H.; Sastrosoewignjo, R.I.; Imai, M.; Miyakawa, Y.; M
. Gen. Virol. 69, 2575-2583, 1988
;Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of surfa
;Reference number: J0253; MUID:89010694; PMID:3171552
;Accession: J0604
;Status: translation not shown
;Molecule type: DNA
;Residues: 1-154 <OKA>
;Cross-references: GB:D00331; NID:g221499
;Genetics:
;Gene: X
;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 42; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
|||||
DB 102 AMSTTDLEA 110

RESULT 13
S35529
ene X protein - hepatitis B virus (subtype adr)
;Species: hepatitis B virus, HBV
```


A:Variety: subtype adr
 C:Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
 C:Accession: S35529
 R:Mukaiide, M.; Kumazawa, T.; Hoshi, A.; Kawaguchi, R.; Hikiji, K.
 Nucleic Acids Res. 20, 6105, 1992
 A:Title: The complete nucleotide sequence of hepatitis B virus, subtype adr (SPADR) and
 A:Reference number: S35527; MUID:93096607; PMID:1461746
 A:Accession: S35529
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-154 <UNK>
 A:Cross-references: EMBL:D12980; NID:G221500; PID:BAA02356.1; PID:G221503
 A:Experimental source: subtype adr
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
 C:Genetics:
 A:Gene: X
 C:Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 42; DB 2; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.075;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 |||||
 Db 102 AMSTTDLEA 110

RESULT 14

S33687
 gene X protein - hepatitis B virus (subtype adw2, patient A938)
 C:Species: hepatitis B virus, HBV
 A:Variety: subtype adw2, patient A938
 C:Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 07-May-1999
 C:Accession: S33687
 R:Preisler-Adams, S.; Schlager, H.J.; Peters, T.; Korp, R.; Rasenack, J.
 Nucleic Acids Res. 21, 2258, 1993
 A:Title: Complete nucleotide sequence of a hepatitis B virus, subtype adw2, and identifi
 A:Reference number: S33686; MUID:93275766; PMID:8502574
 A:Accession: S33687
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-154 <PRE>
 A:Cross-references: EMBL:X70185
 A:Experimental source: subtype adw2, patient A938
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
 C:Genetics:
 A:Gene: X
 C:Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 42; DB 2; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.075;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 AMSTTDLEA 9
 |||||
 Db 102 AMSTTDLEA 110

RESULT 15

S12542
 gene X protein - hepatitis B virus
 C:Species: hepatitis B virus, HBV
 C:Date: 21-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 16-Feb-1997
 C:Accession: S12542
 R:Unger, T.; Shaul, Y.
 VBO J. 9, 1889-1895, 1990
 A:Title: The X protein of the hepatitis B virus acts as a transcription factor when targ
 A:Reference number: S12542; MUID:90269224; PMID:2347309
 A:Accession: S12542
 A:Molecule type: DNA
 A:Residues: 1-154 <UNG>
 C:Genetics:
 A:Gene: X

C:Superfamily: hepatitis B virus gene X protein
 Query Match 100.0%; Score 42; DB 2; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.075;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 |||||
 Db 102 AMSTTDLEA 110

Search completed: December 23, 2003, 08:41:07
 Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 6.4 seconds
(without alignments)
66.131 Million cell updates/sec

Title: US-09-989-621-3
Perfect score: 42
Sequence: 1 AMSTTDLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Databases : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	100.0	154	1 X HPBV2	P03166 hepatitis b
2	42	100.0	154	1 X HPBV4	P12936 hepatitis b
3	42	100.0	154	1 X HPBV9	P17102 hepatitis b
4	42	100.0	154	1 X HPBV1	P20975 hepatitis b
5	42	100.0	154	1 X HPBVJ	P20976 hepatitis b
6	42	100.0	154	1 X HPBVC	P20977 hepatitis b
7	42	100.0	154	1 X HPBVY	P03165 hepatitis b
8	38	90.5	154	1 X HPBVA	P24026 hepatitis b
9	35	83.3	203	1 YNU3 YEAST	P40163 saccharomyc
10	33	78.6	190	1 ARF GIALA	P28991 giardia lam
11	33	78.6	526	1 SECD_HELPJ	Q92J66 helicobacte
12	32	76.2	147	1 RL11_TRETH	P36238 thermus the
13	32	76.2	503	1 SECD_HELPY	O26074 helicobacte
14	32	76.2	506	1 AER_ECOLI	P50466 escherichia
15	31	73.8	402	1 OXAI YEAST	P33952 saccharomyc
16	31	73.8	465	1 YK71_CAEEL	P34318 caenorhabdi
17	31	73.8	1163	1 LEPB_HUMAN	Q9MY10 macaca mula
18	31	73.8	1165	1 LEPB_HUMAN	P48357 homo sapien
19	30	71.4	479	1 RP54_XANCV	P77998 xanthomonas
20	30	71.4	508	1 Y202_HUMAN	P32417 oryctolagus
21	30	71.4	530	1 FMO3_RABIT	O10365 orgyia pseu
22	30	71.4	644	1 VP74_NPVOP	P32417 oryctolagus
23	30	71.4	794	1 YG2A YEAST	Q02061 schizosacch
24	30	71.4	1210	1 RP52_SCHPO	Q10571 homo sapien
25	30	71.4	1319	1 MN1_HUMAN	P36252 thermotoga
26	30	71.4	1690	1 RPOC_THEVA	P12912 hepatitis b
27	29	69.0	154	1 X HPBV1	Q96252 arabidopsis
28	29	69.0	203	1 ATP4_ARATH	P17720 artemia sal
29	29	69.0	229	1 ARTM_ARTSA	P21625 spiroplasma
30	29	69.0	241	1 SPIR_SPIVE	Q94C59 listeria in
31	29	69.0	305	1 MIAA_LISIN	P78697 kluyveromyc
32	29	69.0	320	1 DMI_KULLA	P22193 schizosacch
33	29	69.0	323	1 RAD1_SCHPO	

34 29 69.0 337 1 YKP1_YEAST
35 29 69.0 399 1 OPS2_PATYE
36 29 69.0 406 1 TRPB_CAUCR
37 29 69.0 433 1 DHOM_SYNY3
38 29 69.0 437 1 VPS4_YEAST
39 29 69.0 471 1 ATPB_HERAU
40 29 69.0 495 1 CRTD_RHOSH
41 29 69.0 743 1 CUL2_CABEL
42 29 69.0 922 1 YKFO_YEAST
43 29 69.0 1267 1 DHR1_YEAST
44 28 66.7 109 1 RL37_TETTH
45 28 66.7 129 1 YQ09_HALN1

ALIGNMENTS

RESULT 1
X HPBV2
ID X HPBV2 STANDARD; PRT; 154 AA.
AC P03166; P12935;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw2), and
OC Hepatitis B virus (subtype adw).
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10408, 106821;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ADW2;
RA Valenzuela P., Quiroga M., Zaldivar J., Gray P., Rutter W.J.;
RL (In) Field B.N., Jaenisch R., Fox C.F. (eds.);
RL Animal virus genetics, pp.57-70, Academic Press, New York (1980).
RW [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ADW;
RX MEDLINE=89045656; PubMed=3188399;
RA Lo S.J., Chien M.L., Lee Y.H.W.;
RT "Characteristics of the X gene of hepatitis B virus";
RL Virology 167:289-292 (1988).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ADW;
RX MEDLINE=83168919; PubMed=6300776;
RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
DNA; subtype adr and adw";
RL Nucleic Acids Res. 11:1747-1757 (1983).
RW [4]
CC FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
CC
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CC EMBL; X02763; CAA86540.1; -;
CC EMBL; Z35717; CAA84789.1; -;
CC EMBL; M23692; AAA56820.1; -;
CC PIR; A31289; QQVLAW.
CC PIR; S47408; S47408.
CC InterPro; IPR000236; TransactX.
CC Pfam; PF00739; X; 1.
CC CONFLICT 80 80 E -> A (IN REF. 3).
CC CONFLICT 115 115 C -> S (IN REF. 2).
CC CONFLICT 130 131 KV -> MI (IN REF. 3).
CC SEQUENCE 154 AA; 16583 MW; 7F2AE32AF025670 CRC64;

```

Query Match      100.0%; Score 42; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 102 AMSTTDLEA 110

RESULT 2
X HPBV4
ID X HPBV4 STANDARD; PRT; 154 AA.
AC P12936;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adr4).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10409;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83246570; PubMed=6306594;
RA Fujiyama A., Miyanochara A., Nozaki C., Yoneyama T., Ohtomo N.,
RA Matsubara K.;
RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype
RT adr.";
RL Nucleic Acids Res. 11:4601-4610(1983).
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
CC
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CC
CC EMBL; X01587; CAA25744.1; -
CC InterPro; IPR000236; TransactX.
CC Pfam; PF00739; X; 1.
CC SEQUENCE 154 AA; 16622 MW; 594A1D0718928804 CRC64;

Query Match      100.0%; Score 42; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 102 AMSTTDLEA 110

RESULT 3
X HPBV9
ID X HPBV9 STANDARD; PRT; 154 AA.
AC P17102;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adr / strain 991).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10410;
RN [1]
RP SEQUENCE FROM N.A.
RX Koechel H.G., Schueler A., Lottmann S., Thomassen R.;
RA Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
CC
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CC
CC EMBL; X51970; CAA36231.1; -
CC InterPro; IPR000236; TransactX.
CC Pfam; PF00739; X; 1.
CC SEQUENCE 154 AA; 16553 MW; 52A0D9CEFE6DCDE0 CRC64;

Query Match      100.0%; Score 42; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 102 AMSTTDLEA 110

RESULT 4
X HPBVI
ID X HPBVI STANDARD; PRT; 154 AA.
AC P20975;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adr / strain Indonesia/p1DW420).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10412;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tada F., Sakugawa H., Sastrosewignjo R.I., Imai M.,
RA Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
CC
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CC
CC EMBL; D00331; -; NOT_ANNOTATED_CDS.
CC PIR; JSC604; JS0604.
CC InterPro; IPR000236; TransactX.
CC Pfam; PF00739; X; 1.
CC SEQUENCE 154 AA; 16556 MW; C80C817B961BFFB9 CRC64;

Query Match      100.0%; Score 42; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 102 AMSTTDLEA 110

RESULT 5
X HPBVJ
ID X HPBVJ STANDARD; PRT; 154 AA.
AC P20976;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

```

01-NOV-1995 (Rel. 32, Last annotation update)
 Trans-activating protein X.
 Hepatitis B virus (subtype adw / strain Japan/pJDW233).
 Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 NCBI_TaxID=10413;
 [1]
 RN SEQUENCE FROM N.A.
 MEDLINE=89010694; PubMed=3171552;
 Okamoto H., Tsuda F., Sakugawa H., Sastrosoewignjo R.I., Imai M.,
 Miyakawa Y., Mayumi M.,
 "Typing hepatitis B virus by homology in nucleotide sequence:
 comparison of surface antigen subtypes.",
 J. Gen. Virol. 69:2575-2583(1988).
 CC -1- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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 CC
 DR EMBL; D00329; -; NOT ANNOTATED_CDS.
 DR PIR; JS0256; JS0256.
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 SQ SEQUENCE 154 AA; 16585 MW; 512A5A077169DSCA CRC64;
 Query Match 100.0%; Score 42; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AMSTTDLEA 9
 Db 102 AMSTTDLEA 110
 RESULT 6
 X HPBVO STANDARD; PRT; 154 AA.
 ID X HPBVO
 AC P20977;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Trans-activating protein X.
 DE X.
 OS Hepatitis B virus (subtype adw / strain Okinawa/pODW282).
 OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 NCBI_TaxID=10415;
 [1]
 RN SEQUENCE FROM N.A.
 MEDLINE=89010694; PubMed=3171552;
 Okamoto H., Tsuda F., Sakugawa H., Sastrosoewignjo R.I., Imai M.,
 Miyakawa Y., Mayumi M.,
 "Typing hepatitis B virus by homology in nucleotide sequence:
 comparison of surface antigen subtypes.",
 J. Gen. Virol. 69:2575-2583(1988).
 CC -1- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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 CC
 DR EMBL; D00330; -; NOT ANNOTATED_CDS.
 DR PIR; JS0603; JS0603.
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.

SQ SEQUENCE 154 AA; 16558 MW; E2646C059A30125F CRC64;
 Query Match 100.0%; Score 42; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AMSTTDLEA 9
 Db 102 AMSTTDLEA 110
 RESULT 7
 X HPBVI STANDARD; PRT; 154 AA.
 ID X HPBVI
 AC P03165;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Trans-activating protein X.
 DE X.
 OS Hepatitis B virus (subtype ayw).
 OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 NCBI_TaxID=10418;
 [1]
 RN SEQUENCE FROM N.A.
 MEDLINE=8102091; PubMed=399327;
 Galibert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.,
 "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)
 cloned in E. coli.",
 Nature 281:646-650(1979).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Latvia;
 RX MEDLINE=85204397; PubMed=3996597;
 Richko V., Dreilina D., Pushko P.M., Pumpen P.P., Gren E.,
 "Subtype ayw variant of hepatitis B virus. DNA primary structure
 analysis.",
 FEBS Lett. 185:208-212(1985).
 CC -1- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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 CC
 DR EMBL; V01460; -; NOT ANNOTATED_CDS.
 DR EMBL; X02496; CAB41697.1; -;
 DR PIR; A03719; QOVLBI.
 DR PIR; A05237; QOVLBI.
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 FT VARIANT 46 46 P -> S (IN STRAIN LATVIA).
 FT VARIANT 84 88 NAHQI -> KAQPF (IN STRAIN LATVIA).
 FT VARIANT 102 102 A -> V (IN STRAIN LATVIA).
 FT CONFLICT 26 26 R -> C (IN REF. 1)
 SQ SEQUENCE 154 AA; 16618 MW; 29FDCC9E09A34B5 CRC64;
 Query Match 100.0%; Score 42; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AMSTTDLEA 9
 Db 102 AMSTTDLEA 110
 RESULT 8
 X HPBVA STANDARD; PRT; 154 AA.
 ID X HPBVA
 AC P24026;

DT 01-VAR-1992 (Rel. 21, Created)
 DT 01-VAR-1992 (Rel. 21, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 GN Trans-activating protein X.
 DE
 OS Hepatitis B virus (strain alpha).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10411;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90266476; PubMed=2345966;
 RA Tong S., Li J., Vitvitski L., Trepo C.;
 RT "Active hepatitis B virus replication in the presence of anti-HBe is
 associated with viral variants containing an inactive pre-C region.";
 RL Virology 176:596-603(1990)
 CC
 CC 1- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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 CC
 CC EMBL; M32138; AAA4504.1; -
 DR PIR; D34773; QOVLAI.
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 SQ SEQUENCE 154 AA; 16671 MW; 2CPEEA77FA5E271F CRC64;
 Query Match 90.5%; Score 38; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 MSTTDLEA 9
 DB 103 MSTTDLEA 110
 RESULT 9
 YNU3 YEAST
 ID YNU3 YEAST STANDARD; PRT; 203 AA.
 AC P40163;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Very hypothetical 22.4 kDa protein in SPX18-SPX19 intergenic region.
 GN YNL203C OR N1358.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OX NCBI_TaxID=4932;
 RN
 RP SEQUENCE FROM N.A.
 RX STRAIN=S288c / FV1679;
 RA Jomiaux J.-L., Coster F., Fournelle B., Goffeau A.;
 RT "A 21.7 kb DNA segment on the left arm of yeast chromosome XIV
 carries WHR3, GCR2, SPX18, an homologue to the heat shock gene
 SSRI and 8 new open reading frames of unknown function.";
 RL Yeast 10:1639-1645(1994).
 CC
 CC 1- FUNCTION: UNKNOWN.
 CC
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 CC EMBL; X78898; CAA55505.1; -
 DR EMBL; Z71479; CAA96102.1; -
 DR EMBL; M90351; -; NOT_ANNOTATED_CDS.
 DR PIR; S50728; S50728.
 DR SGD; S0005147; YNL203C.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 89 109 POTENTIAL.
 FT CONFLICT 160 160 S -> F (IN REF. 2).
 FT CONFLICT 178 178 Y -> H (IN REF. 2).
 FT CONFLICT 183 183 X -> T (IN REF. 2).
 FT CONFLICT 186 186 F -> L (IN REF. 2).
 SQ SEQUENCE 203 AA; 22418 MW; C22CE2651E0925BB CRC64;
 Query Match 83.3%; Score 35; DB 1; Length 203;
 Best Local Similarity 77.8%; Pred. No. 1-2;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AMSTTDLEA 9
 DB 23 SMSTTDLEA 31
 RESULT 10
 ARF GIALA
 ID ARF GIALA STANDARD; PRT; 190 AA.
 AC P26991;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ADP-ribosylation factor
 OS Giardia lamblia (Giardia intestinalis)
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
 OX NCBI_TaxID=5741;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92250616; PubMed=1577802;
 RA Murtagh J.J. Jr., Mowatt M.W., Lee C.-M., Lee F.-J.S., Mishima K.,
 RA Nash T.E., Moss J., Vaughan M.;
 RT "Guanine nucleotide-binding proteins in the intestinal parasite
 Giardia lamblia. Isolation of a gene encoding an approximately 20-kDa
 ADP-ribosylation factor.";
 RL J. Biol. Chem. 267:9654-9662(1992).
 CC 1- FUNCTION: GTP-BINDING PROTEIN THAT FUNCTIONS AS AN ALLOSTERIC
 CC ACTIVATOR OF THE CHOLERA TOXIN CATALYTIC SUBUNIT, AN ADP-
 CC RIBOSYLTRANSFERASE. INVOLVED IN PROTEIN TRAFFICKING; MAY MODULATE
 CC VESICLE BUDDING AND UNCOATING WITHIN THE GOLGI APPARATUS.
 CC 1- SIMILARITY: BELONGS TO THE ARF FAMILY OF GTP-BINDING PROTEINS.
 CC
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 CC
 CC EMBL; M86513; -; NOT_ANNOTATED_CDS.
 DR PIR; S29008; S29008.
 DR HSP; P32889; 1RSP.
 DR InterPro; IPR006688; ARF.
 DR InterPro; IPR006689; ARF/SAR.
 DR InterPro; IPR001806; Ras transfrmg.
 DR InterPro; IPR005225; Small_GTP.
 DR Pfam; PF00025; arf; 1.
 DR PRINTS; PR00449; RASTENFERMNG.
 DR PRINTS; PR00328; SARLGTBP.
 DR SMART; SM00177; ARF; 1.
 DR TIGRfam; TIGR00031; small_GTP; 1.
 DR PROSITE; PS01019; ARF; 1.
 DR GTP-binding; Myristate; Protein transport; Golgi stack.
 KW INIT_MET 0 0 BY SIMILARITY.
 FT

FT LIPID 1 1 MYRISTATE (POTENTIAL).
 FT NP_BIND 23 30 GTP (BY SIMILARITY).
 FT NP_BIND 66 70 GTP (BY SIMILARITY).
 FT NP_BIND 127 130 GTP (BY SIMILARITY).
 SQ SEQUENCE 190 AA; 21634 MW; B05549FA0DA49036 CRC64;
 Query Match 78.6%; Score 33; DB 1; Length 190;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AMSTTDL 7
 DB 134 AMSTTDL 140
 RESULT 11
 ID _SCD_HELPJ STANDARD; PRT; 526 AA.
 AC Q3ZJ66;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein-export membrane protein.
 GN SCD OR JHP1449.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Helicobacter.
 OX NCBI_TaxID=85963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed=9923682;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
 RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 RA Gibson R., Merberg D., Malls S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 RA Trust T.J.,
 RT Genomic sequence comparison of two unrelated isolates of the human
 RT gastric pathogen Helicobacter pylori.
 RL Nature 397:176-180(1999).
 CC -1- FUNCTION: INVOLVED IN PROTEIN EXPORT (BY SIMILARITY).
 CC -1- SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS
 CC WHICH COMPRISE SECA, SECB, SECD, SECE, SECF, SECG AND SECH
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SECD/SECF FAMILY. SECD FAMILY.
 CC -----
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 CC -----
 CC EMBL; A5001567; AAD07024.1; -
 CC PIR; D71805; D71805.
 CC InterPro; IPR001036; Acrlvin_res.
 CC InterPro; IPR005791; Secd.
 CC InterPro; IPR003335; Secd.
 CC Pfam; PF02355; Secd Secf.
 CC PRINTS; PR00702; ACRIFLAVINRP.
 CC TIGRFAMs; TIGR00916; 2A0604501; 1.
 CC TIGRFAMs; TIGR01129; secd; 1.
 CC Protein transport; Translocation; Transmembrane; Membrane;
 CC Complete proteome.
 FT TRANSMEM 8 28 POTENTIAL.
 FT TRANSMEM 356 376 POTENTIAL.
 FT TRANSMEM 379 399 POTENTIAL.
 FT TRANSMEM 453 473 POTENTIAL.
 FT TRANSMEM 478 498 POTENTIAL.
 SQ SEQUENCE 526 AA; 56796 MW; 5B4C9E505794782A CRC64;
 Query Match 78.6%; Score 33; DB 1; Length 526;

Best Local Similarity 77.8%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AMSTTDL 9
 DB 208 AMSTTDL 216
 RESULT 12
 ID RL11 THETH STANDARD; PRT; 147 AA.
 AC P36238;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 50S ribosomal protein L11.
 GN RPLK OR RPL11.
 OS Thermus thermophilus.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 OX NCBI_TaxID=274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VKI;
 RA Ossina N., Eliseikina I., Garber M.B., Jonsson B.-H.;
 RL Submitted (SFP-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-40 FROM N.A.
 RC STRAIN=HB8 / ATCC 27634;
 RX MEDLINE=93077476; PubMed=1447157;
 RA Heinrich T., Schroeder W., Erdmann V.A., Hartmann R.K.;
 RT "Identification of the gene encoding transcription factor NusG of
 RT Thermus thermophilus".
 RL J. Bacteriol. 174:7859-7863(1992).
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE L11P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 CC EMBL; X81375; CAA57138.1; -
 CC HSRP; P29395; LWS.
 CC InterPro; IPR000911; Ribosomal L11.
 CC InterPro; IPR006519; Ribosomal L11bac.
 CC Pfam; PF00298; Ribosomal L11; 1.
 CC Pfam; PF01946; Ribosomal L11_N; 1.
 CC ProDom; PD001367; Ribosomal_L11; 1.
 CC SMART; SM00849; RL11; 1.
 CC TIGRFAMs; TIGR01632; L11_bact; 1.
 CC PROSITE; PS00359; RIBOSOMAL_L11; 1.
 CC Ribosomal protein; RNA-binding.
 CC VARIANT 23 23 V -> G (IN STRAIN HB8).
 SQ SEQUENCE 147 AA; 15505 MW; 3D8ECBEB85B5FE9 CRC64;
 Query Match 76.2%; Score 32; DB 1; Length 147;
 Best Local Similarity 75.0%; Pred. No. 4.1;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MSTTDL 9
 DB 115 MNTTDL 122
 RESULT 13
 SECD_HELPJ
 ID _SCD_HELPJ STANDARD; PRT; 503 AA.
 AC Q26074;

DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein-export membrane protein secD.
 GN SEC02 OR HP1550.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Helicobacter.
 OX NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=26695 / ATCC 700392;
 RX MEDLINE=97394467; PubMed=9521185;
 RA Tomb J.-F., White O., Karlavage A.R., Clayton R.A., Sutton G.G., Burland V.,
 RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
 RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
 RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glöck A.,
 RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
 RA Berg D.E., Gocayne J.D., Uterback T.R., Peterson J.D., Kelley J.M.,
 RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Wallin E.,
 RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 RA Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen Helicobacter
 pylori.";
 RL Nature 388:539-547(1997).
 CC -!- FUNCTION: INVOLVED IN PROTEIN EXPORT (BY SIMILARITY).
 CC -!- SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLLOCATION APPARATUS
 CC WHICH COMPRISE SECA, SECB, SECD, SECE, SECF, SECG AND SECH
 CC (BY SIMILARITY)
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE SECY/SECF FAMILY. SEC02 FAMILY.
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 CC
 CC EMBL; AF000652; AAD08588.1; --
 CC PIR; F64713; F64713.
 CC TIGR; HP1550; --
 CC InterPro; IPR001036; Acrlvin_res.
 CC InterPro; IPR005791; SecD.
 CC InterPro; IPR003335; SecD_SecF.
 CC Pfam; PF02355; SecD_SecF; 1.
 CC PRINTS; PR00702; ACRIFLAVINRP.
 CC TIGRFAMs; TIGR00916; 2A0604s01; 1.
 CC TIGRFAMs; TIGR01129; secD; 1.
 CC Protein transport; Translocation; Membrane;
 KW Complete proteome.
 FT TRANSMEM 199 219 POTENTIAL.
 FT TRANSMEM 334 354 POTENTIAL.
 FT TRANSMEM 357 377 POTENTIAL.
 FT TRANSMEM 383 403 POTENTIAL.
 FT TRANSMEM 456 476 POTENTIAL.
 SQ SEQUENCE 503 AA; 54247 MW; 8541C291CA317086 CRC64;
 Query Match 76.2%; Score 32; DB 1; Length 503;
 Best Local Similarity 77.8%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AMSTTDLEA 9
 Db 186 AMKMTDLEA 194
 RESULT 14
 AER_ECOLI STANDARD; PRT; 506 AA.
 ID AER_ECOLI
 AC P50466.
 DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Aerotaxis receptor.
 GN AER OR AIR OR B3072.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP FUNCTION
 RX MEDLINE=97334134; PubMed=9190831;
 RA Bibikov S.I., Biran R., Rudd K.E., Parkinson J.S.;
 RT "A signal transducer for aerotaxis in Escherichia coli.";
 RL J. Bacteriol. 179:4075-4079(1997).
 RN [3]
 RP FUNCTION
 RX MEDLINE=98021405; PubMed=9380671;
 RA Rebapragada A., Johnson M.S., Harding G.P., Zuccarelli A.J.,
 RA Fletcher H.M., Zhulin I.B., Taylor B.L.;
 RT "The Aer protein and the serine chemoreceptor Tsr independently sense
 RT intracellular energy levels and transduce oxygen, redox, and energy
 RT signals for Escherichia coli behavior.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:10541-10546(1997).
 CC -!- FUNCTION: SIGNAL TRANSDUCER FOR AEROTAXIS. THE AEROTACTIC
 CC RESPONSES IS THE ACCUMULATION OF CELLS AROUND AIR BUBBLES. THE
 CC NATURE OF THE SENSORY STIMULUS DETECTED BY THIS PROTEIN IS THE
 CC PROTON MOTIVE FORCE OR CELLULAR REDOX STATE. IT USES A PAD
 CC PROSTHETIC GROUP AS A REDOX SENSOR TO MONITOR OXYGEN LEVELS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC (POTENTIAL).
 CC -!- SIMILARITY: IN THE N-TERMINAL TO NIFL AND FIXL AND OTHER PROTEINS
 CC IMPLICATED IN OXYGEN-SENSING.
 CC -!- SIMILARITY: Contains 1 methyl-accepting transducer domain.
 CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
 CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
 CC
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 CC EMBL; U28379; AA89151.1; --
 CC EMBL; A5000389; AAC76107.1; --
 CC PIR; E65095; E65095.
 CC HSP; P02942; 1Q07.
 CC EcoGene; EGI2955; aer.
 CC InterPro; IPR004089; Chmtaxis_transd.
 CC InterPro; IPR003660; HAMF.
 CC InterPro; IPR004090; Me_chmtaxis.
 CC InterPro; IPR001610; PAC.
 CC InterPro; IPR000014; PAS_domain.
 CC Pfam; PF00672; HAMF; 1.
 CC Pfam; PF00015; MCPsignal; 1.
 CC Pfam; PF00785; PAC; 1.
 CC PRINTS; PR00260; CHEMTRNSDUCC.
 CC SMART; SM00283; WA; 1.
 CC SMART; SM00086; PAC; 1.
 CC SMART; SM00091; PAC; 1.
 CC TIGRFAMs; TIGR00229; sensory_box; 1.
 CC PROSITE; PS50111; CHEMOTAXIS_TRANSDCU_2; 1.

KW Chemotaxis; Transducer; Transmembrane; Methylation; Periplasmic;
 KW Inner membrane; FAD; Transproteins; Complete proteome.
 FT DOMAIN 1 166 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 167 186 POTENTIAL.
 FT DOMAIN 187 190 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 191 209 POTENTIAL.
 FT DOMAIN 210 506 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 263 492 METHYL-ACCEPTING TRANSFERASE.
 SQ SEQUENCE 506 AA; 55065 MW; 913DEBCF14E3FD08 CRC64;
 Query Match 76.2%; Score 32; DB 1; Length 506;
 Best Local Similarity 75.0%; Pred. No. 17;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MSTTDLQA 9
 DB 21 MSTTDLQS 28
 RESULT 15
 OXAL YEAST STANDARD; PRT; 402 AA.
 ID OXAL YEAST STANDARD; PRT; 402 AA.
 AC P39952; 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Cytochrome oxidase biogenesis protein OXAL, mitochondrial precursor.
 GN OXAL OR PRT1402 OR YER154W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OC NCBI_TaxID=4932;
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:58 ; Search time 23.6 Seconds
(without alignments)
98.410 Million cell updates/sec

Title: US-09-989-621-3
Perfect score: 42
Sequence: 1 AMSTTDLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL 23:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	42	100.0	58	12 Q9E0Q4	Q9E0Q4 hepatitis b
2	42	100.0	58	12 Q9E0P6	Q9E0P6 hepatitis b
3	42	100.0	58	12 Q9E0U2	Q9E0U2 hepatitis b
4	42	100.0	58	12 Q9E0S4	Q9E0S4 hepatitis b
5	42	100.0	58	12 Q9E0P2	Q9E0P2 hepatitis b
6	42	100.0	58	12 Q9E0S6	Q9E0S6 hepatitis b
7	42	100.0	58	12 Q9E0U0	Q9E0U0 hepatitis b
8	42	100.0	58	12 Q9E0Q2	Q9E0Q2 hepatitis b
9	42	100.0	58	12 Q9E0S2	Q9E0S2 hepatitis b
10	42	100.0	58	12 Q9E0W6	Q9E0W6 hepatitis b
11	42	100.0	58	12 Q9E0R4	Q9E0R4 hepatitis b
12	42	100.0	58	12 Q9E0P0	Q9E0P0 hepatitis b
13	42	100.0	58	12 Q9E0V2	Q9E0V2 hepatitis b
14	42	100.0	58	12 Q9E0U8	Q9E0U8 hepatitis b
15	42	100.0	58	12 Q9E0W0	Q9E0W0 hepatitis b
16	42	100.0	58	12 Q9E0U4	Q9E0U4 hepatitis b

17	42	100.0	58	12 Q9E0T0	Q9E0T0 hepatitis b
18	42	100.0	58	12 Q9E0N6	Q9E0N6 hepatitis b
19	42	100.0	58	12 Q9E0V6	Q9E0V6 hepatitis b
20	42	100.0	58	12 Q9E0P8	Q9E0P8 hepatitis b
21	42	100.0	58	12 Q9E0R0	Q9E0R0 hepatitis b
22	42	100.0	58	12 Q9E0R2	Q9E0R2 hepatitis b
23	42	100.0	58	12 Q9E0V0	Q9E0V0 hepatitis b
24	42	100.0	58	12 Q9E0T8	Q9E0T8 hepatitis b
25	42	100.0	58	12 Q9E0R6	Q9E0R6 hepatitis b
26	42	100.0	58	12 Q9E0T6	Q9E0T6 hepatitis b
27	42	100.0	58	12 Q9E0N8	Q9E0N8 hepatitis b
28	42	100.0	58	12 Q9E0U6	Q9E0U6 hepatitis b
29	42	100.0	58	12 Q9E0Q6	Q9E0Q6 hepatitis b
30	42	100.0	58	12 Q9E0W4	Q9E0W4 hepatitis b
31	42	100.0	58	12 Q9E0S0	Q9E0S0 hepatitis b
32	42	100.0	58	12 Q9E0V8	Q9E0V8 hepatitis b
33	42	100.0	60	12 Q8V787	Q8V787 hepatitis b
34	42	100.0	129	12 Q8QVU1	Q8QVU1 hepatitis b
35	42	100.0	129	12 Q8QVU0	Q8QVU0 hepatitis b
36	42	100.0	129	12 Q8QVU5	Q8QVU5 hepatitis b
37	42	100.0	129	12 Q8QVT1	Q8QVT1 hepatitis b
38	42	100.0	129	12 Q8QVU2	Q8QVU2 hepatitis b
39	42	100.0	129	12 Q8QVT3	Q8QVT3 hepatitis b
40	42	100.0	129	12 Q8QVT0	Q8QVT0 hepatitis b
41	42	100.0	129	12 Q8QVT4	Q8QVT4 hepatitis b
42	42	100.0	129	12 Q8QVS9	Q8QVS9 hepatitis b
43	42	100.0	129	12 Q8QVT7	Q8QVT7 hepatitis b
44	42	100.0	129	12 Q8QVT2	Q8QVT2 hepatitis b
45	42	100.0	129	12 Q8QVT6	Q8QVT6 hepatitis b

ALIGNMENTS

RESULT 1
Q9E0Q4 PRELIMINARY; PRT; 58 AA.
AC Q9E0Q4;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]_TaxID=10407;
RP SEQUENCE FROM N.A.
RC STRAIN=BBECO324;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls".
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289966; AAG25271.1; -
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
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Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AMSTTDLEA 9
Db 6 AMSTTDLEA 14
RESULT 2
Q9E0P6 PRELIMINARY; PRT; 58 AA.
ID Q9E0P6
AC Q9E0P6;

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DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBSC0115;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289970; AAG25233.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON-TER
SQ SEQUENCE 58 AA; 6464 MW; 195CADD9A4A848F4 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
Db |||||
6 AMSTTDLEA 14

RESULT 3
Q9E0U2 PRELIMINARY; PRT; 58 AA.
AC Q9E0U2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBSC0115;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289970; AAG25233.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON-TER
SQ SEQUENCE 58 AA; 6487 MW; 049D70C1351248F4 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
Db |||||
6 AMSTTDLEA 14

RESULT 4
Q9E0S4 PRELIMINARY; PRT; 58 AA.
AC Q9E0S4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

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DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBSC0138;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289956; AAG25251.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
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Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
Db |||||
6 AMSTTDLEA 14

RESULT 5
Q9E0P2 PRELIMINARY; PRT; 58 AA.
AC Q9E0P2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
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RC STRAIN=BBSC0380;
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RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289972; AAG25283.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON-TER
SQ SEQUENCE 58 AA; 6490 MW; 195CACC1351248F4 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
Db |||||
6 AMSTTDLEA 14

RESULT 6
Q9E0S6 PRELIMINARY; PRT; 58 AA.
AC Q9E0S6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.

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DC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
CX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBSC0152;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RL HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289955; AAG25249.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
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SQ SEQUENCE 58 AA; 6487 MW; 485DACC1351248E8 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 AMSTTDLEA 9
| | | | |
b 6 AMSTTDLEA 14

RESULT 7
ID Q9E0U0 PRELIMINARY; PRT; 58 AA.
AC Q9E0U0;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
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RP SEQUENCE FROM N.A.
RC STRAIN=BBSC0148;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RL HBV Isolated from Patients with Hepatocellular Carcinoma and
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RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289948; AAG25235.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 58 AA; 6487 MW; 049D70C1351248F4 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 AMSTTDLEA 9
| | | | |
b 6 AMSTTDLEA 14

RESULT 8
ID Q9E0Q2 PRELIMINARY; PRT; 58 AA.
AC Q9E0Q2;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBSC0152;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RL HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289955; AAG25249.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 58 AA; 6487 MW; 485DACC1351248E8 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 AMSTTDLEA 9
| | | | |
b 6 AMSTTDLEA 14

RESULT 9
ID Q9E0S2 PRELIMINARY; PRT; 58 AA.
AC Q9E0S2;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBSC0308;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RL HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289957; AAG25253.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 58 AA; 6494 MW; B8B3BDD34DF48FF CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 AMSTTDLEA 9
| | | | |
b 6 AMSTTDLEA 14

RESULT 10
ID Q9E0W6 PRELIMINARY; PRT; 58 AA.
AC Q9E0W6;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBSC033;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
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RP SEQUENCE FROM N.A.
RC STRAIN=BBSC0354;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RL HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289967; AAG25273.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 58 AA; 6461 MW; 4ED3CADDE4DF48E2 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 AMSTTDLEA 9
| | | | |
b 6 AMSTTDLEA 14

RESULT 9
ID Q9E0S2 PRELIMINARY; PRT; 58 AA.
AC Q9E0S2;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBSC0308;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RL HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289957; AAG25253.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 58 AA; 6494 MW; B8B3BDD34DF48FF CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 AMSTTDLEA 9
| | | | |
b 6 AMSTTDLEA 14

RESULT 10
ID Q9E0W6 PRELIMINARY; PRT; 58 AA.
AC Q9E0W6;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBSC033;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
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RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289935; AAG25209.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER
SQ SEQUENCE 58 AA; 6464 MW; 195CACDA94A848F4 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 6 AMSTTDLEA 14

RESULT 11
Q9E0R4 PRELIMINARY; PRT; 58 AA.
AC Q9E0R4
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BSHCC259;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289961; AAG25261.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER
SQ SEQUENCE 58 AA; 6478 MW; 195CACDDE4DF48F4 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 6 AMSTTDLEA 14

RESULT 12
Q9E0P0 PRELIMINARY; PRT; 58 AA.
AC Q9E0P0
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BSHCC399;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";

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RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289973; AAG25285.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER
SQ SEQUENCE 58 AA; 6478 MW; 195CACDDE4DF48F4 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 6 AMSTTDLEA 14

RESULT 13
Q9E0V2 PRELIMINARY; PRT; 58 AA.
AC Q9E0V2
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BSHCC140;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289942; AAG25223.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER
SQ SEQUENCE 58 AA; 6490 MW; 195CACCI351248F4 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 6 AMSTTDLEA 14

RESULT 14
Q9E0U8 PRELIMINARY; PRT; 58 AA.
AC Q9E0U8
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BSHCC180;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289944; AAG25227.1; -.
DR InterPro; IPR000236; TransactX.

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DR Pfam; PF00739; X; 1. 1
FT NON TER 1
SQ SEQUENCE 58 AA; 6506 MW; B65CACC135125E98 CRC64;
Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2y 1 AMSTTDLEA 9
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2b 6 AMSTTDLEA 14
RESULT 15
29EOWO PRELIMINARY; PRT; 58 AA.
AC Q9EOWO;
JT 01-MAR-2001 (TrEMBLrel. 16, Created)
JT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
JT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (fragment).
EN X.
DS Hepatitis B virus.
DC Viruses; Retroviruses; Hepadnaviridae; Orthohepadnavirus.
DX NCBI_TaxID=10407;
UN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBHCC64;
UA Tagger A., Binelli G., Donato F., Ribero M.L.;
XT "Prevalence of 1762r and 1764A Mutations in the Basic Core Promoter of
XT HBV Isolated from Patients with Hepatocellular Carcinoma and
XT Controls.";
IL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289938; AAG25215.1; -
DR InterPro; IPR000236; TransactX.
RR Pfam; PF00739; X; 1. 1
RT NON TER 1
TQ SEQUENCE 58 AA; 6478 MW; 195CACDDE4DF48F4 CRC64;
Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2y 1 AMSTTDLEA 9
|||
2b 6 AMSTTDLEA 14
Search completed: December 23, 2003, 08:46:10
Job time : 24.6 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:41:18 ; Search time 9.6 Seconds
(without alignments)
39.666 Million cell updates/sec

Title: US-09-989-621-4
Perfect score: 55
Sequence: 1 CLFKDWEEL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	9	4	US-09-051-006-4
2	55	100.0	17	6	5183734-17
3	55	100.0	18	6	5183734-9
4	55	100.0	24	6	5204446-3
5	55	100.0	37	2	US-08-319-376-5
6	55	100.0	154	6	5183734-1
7	52	94.5	24	6	5204446-1
8	52	94.5	24	6	5204446-2
9	52	94.5	153	6	5196194-20
10	52	94.5	154	6	US-09-719-528A-5
11	46	83.6	16	6	5183734-3
12	40	72.7	462	4	US-09-134-001C-3717
13	37	67.3	14	5	PCT-US94-06360-2
14	37	67.3	936	5	PCT-US93-05944-2
15	37	67.3	1008	4	US-09-308-453-2
16	37	67.3	1118	3	US-09-379-523-3
17	36	65.5	307	4	US-09-107-532A-6172
18	36	65.5	334	4	US-09-252-991A-18454
19	35	63.6	587	4	US-09-252-991A-21170
20	35	63.6	1128	4	US-09-328-352-4973
21	35	63.6	1226	4	US-09-601-537-7
22	35	63.6	1227	2	US-08-760-075A-18
23	35	63.6	1227	3	US-09-338-546-18
24	35	63.6	1227	4	US-09-659-084-18
25	34	61.8	141	4	US-09-107-532A-4835
26	34	61.8	209	4	US-09-328-352-7988
27	34	61.8	271	1	US-08-467-155A-10

28	34	61.8	271	2	US-08-628-198-10	Sequence 10, Appl
29	34	61.8	271	3	US-09-201-038-10	Sequence 10, Appl
30	34	61.8	271	5	PCT-US96-07343-10	Sequence 10, Appl
31	34	61.8	286	5	PCT-US92-00282-9	Sequence 9, Appl
32	34	61.8	287	4	US-09-305-856B-10	Sequence 10, Appl
33	34	61.8	630	3	US-08-771-986A-2	Sequence 2, Appl
34	34	61.8	631	4	US-08-769-802A-2	Sequence 2, Appl
35	34	61.8	631	4	US-09-252-991A-26444	Sequence 26444, A
36	34	61.8	752	4	US-09-873-404-2	Sequence 2, Appl
37	34	61.8	752	1	US-08-244-189-2	Sequence 2, Appl
38	34	61.8	823	1	US-08-461-551-2	Sequence 2, Appl
39	34	61.8	823	4	US-09-037-621A-2	Sequence 2, Appl
40	34	61.8	1068	3	US-08-390-874C-11	Sequence 11, Appl
41	34	61.8	1068	4	US-09-265-772-11	Sequence 11, Appl
42	34	61.8	1069	2	US-08-162-081B-37	Sequence 37, Appl
43	34	61.8	1069	3	US-08-780-872-37	Sequence 37, Appl
44	34	61.8	1069	3	US-09-085-957-37	Sequence 37, Appl
45	34	61.8	1080	2	US-08-162-081B-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-09-051-006-4
; Sequence 4, Application US/09051006
; Patent No. 6380359
; GENERAL INFORMATION:
; APPLICANT: Mogam Biotechnology Research Institute
; APPLICANT: Kim, Tae-Young
; APPLICANT: Lee, Ki-Young
; APPLICANT: Chang, Jin-Soo
; APPLICANT: Cho, Sung-Yoo
; APPLICANT: Hwang, Yu-Kyeong
; APPLICANT: Choi, Myeong
; APPLICANT: Cheong, Hong-Seok
; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
; FILE REFERENCE: 0136/0E154
; CURRENT APPLICATION NUMBER: US/09/051.006
; CURRENT FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-051-006-4

Query Match 100.0%; Score 55; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
| | | | | | | | | |
Db 1 CLFKDWEEL 9

RESULT 2
5183734-17
; Patent No. 5183734
; APPLICANT: MORIARTY, ANN M.
; TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
; FOR ASSAYING SV40 HEXAG
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,982
; FILING DATE: 17-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 54,424
; FILING DATE: 26-MAY-1987
; APPLICATION NUMBER: 648,142
; FILING DATE: 07-SEP-1984

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; APPLICATION NUMBER: 587,570
; FILING DATE: 08-MAR-1984
; SEQ ID NO:17:
; LENGTH: 17
5183734-17
Query Match      100.0%; Score 55; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
Db 1 CLFKDWEEL 9

RESULT 3
5183734-9
; Patent No. 5183734
; APPLICANT: MORIARTY, ANN M.
; TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
; FOR ASSAYING SV40 HBXAG
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,982
; FILING DATE: 17-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 54,424
; FILING DATE: 26-MAY-1987
; APPLICATION NUMBER: 648,142
; FILING DATE: 07-SEP-1984
; APPLICATION NUMBER: 587,570
; FILING DATE: 08-MAR-1984
; SEQ ID NO:9:
; LENGTH: 18
5183734-9
Query Match      100.0%; Score 55; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
Db 1 CLFKDWEEL 9

RESULT 4
5204446-3
; Patent No. 5204446
; APPLICANT: KUMAZAWA, TOSHIKAZU, MASATOSHI
; TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY
; WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/503,239
; FILING DATE: 02-APR-1990
; SEQ ID NO:3:
; LENGTH: 24
5204446-3
Query Match      100.0%; Score 55; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
Db 2 CLFKDWEEL 10

RESULT 5
US-08-319-376-5
; Sequence 5, Application US/08319376
; Patent No. 5872206
; GENERAL INFORMATION:
; APPLICANT: Liang, Tsanyang J
; APPLICANT: Huang, Jiakang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INTERFERING
; WITH HEPATITIS B VIRUS INFECTION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,376
; FILING DATE: 06-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Ph.D., Kathleen A.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: MGH-126XX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-319-376-5
Query Match      100.0%; Score 55; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
Db 5 CLFKDWEEL 13

RESULT 6
5183734-1
; Patent No. 5183734
; APPLICANT: MORIARTY, ANN M.
; TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
; FOR ASSAYING SV40 HBXAG
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,982
; FILING DATE: 17-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 54,424
; FILING DATE: 26-MAY-1987
; APPLICATION NUMBER: 648,142
; FILING DATE: 07-SEP-1984
; APPLICATION NUMBER: 587,570
; FILING DATE: 08-MAR-1984
; SEQ ID NO:1:
; LENGTH: 154
5183734-1
Query Match      100.0%; Score 55; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CLFKDWEEL 9
Db 115 CVFKDWEEL 123

RESULT 7
5204446-1
;Patent No. 5204446
; APPLICANT: KUMAZAWA, TOSHIKI;OSANAI, MASATOSHI
; TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY
; WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/503,239
; FILING DATE: 02-APR-1990
; SEQ ID NO:1:
; LENGTH: 24
5204446-1

Query Match 94.5%; Score 52; DB 6; Length 24;
Best Local Similarity 88.9%; Pred. No. 0.013;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
Db 2 CVFKDWEEL 10

RESULT 8
5204446-2
;Patent No. 5204446
; APPLICANT: KUMAZAWA, TOSHIKI;OSANAI, MASATOSHI
; TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY
; WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/503,239
; FILING DATE: 02-APR-1990
; SEQ ID NO:2:
; LENGTH: 24
5204446-2

Query Match 94.5%; Score 52; DB 6; Length 24;
Best Local Similarity 88.9%; Pred. No. 0.013;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
Db 2 CVFKDWEEL 10

RESULT 9
5196194-20
;Patent No. 5196194
; APPLICANT: RUTTER, WILLIAM J.;GOODMAN, HOWARD M.
; TITLE OF INVENTION: VACCINES CONTAINING HEPATITIS B S-PROTEIN
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/679,621
; FILING DATE: 7-DEC-1984
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 513,055
; FILING DATE: 12-JUL-1983
; APPLICATION NUMBER: 107,267
; FILING DATE: 21-DEC-1979
; APPLICATION NUMBER: 41,909
; FILING DATE: 24-MAY-1979
; SEQ ID NO:20:
; LENGTH: 153
5196194-20

Query Match 94.5%; Score 52; DB 6; Length 153;

Best Local Similarity 88.9%; Pred. No. 0.09;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CLFKDWEEL 9
Db 115 CVFKDWEEL 123

RESULT 10
US-09-719-528A-5
; Sequence 5, Application US/09719528A
; Patent No. 6586675
; GENERAL INFORMATION:
; APPLICANT: Oon, Chong Jin
; Lim, Gek Keow
; Zhao, Yi
; Chen, Wei Ning
; TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
; USES THEREOF

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ladas & Parry
STREET: 26 West 61 Street
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10023

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/719,528A
FILING DATE: 30-Apr-2001
CLASSIFICATION: 435

Prior APPLICATION DATA:
APPLICATION NUMBER: PCT/SG98/00046
FILING DATE: 19-JAN-1998

ATTORNEY/AGENT INFORMATION:
NAME: Mass, Clifford J.

REGISTRATION NUMBER: 30,086
REFERENCE/DOCKET NUMBER: U-013109-7

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 708-1800

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-719-528A-5

Query Match 94.5%; Score 52; DB 4; Length 154;
Best Local Similarity 88.9%; Pred. No. 0.091;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
Db 115 CVFKDWEEL 123

RESULT 11
5183734-3
;Patent No. 5183734
; APPLICANT: MORIARTY, ANN M.
; TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
; FOR ASSAYING SV40 HEXAG
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,982
; FILING DATE: 17-JUL-1990


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; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/074,346
; FILING DATE: June 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: JEFF-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: Amino Acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; ANTI-SENSE: NO
; PCT-US94-06360-2
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; Query Match 67.3%; Score 37; DB 5; Length 14;
; Best Local Similarity 100.0%; Pred. No. 2.7;
; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 2 LFKDWE 7
; DB 1 LFKDWE 6
;
; RESULT 14
; PCT-US93-05944-2
; Sequence 2, Application PC/TUS9305944
; GENERAL INFORMATION:
; APPLICANT: Lin et al., Hun-Chi
; TITLE OF INVENTION: Molecular cloning of the genes
; NUMBER OF INVENTION: responsible for collagenase product
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Harris Brotman
; STREET: 401 B. St Ste 1700
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05944
; FILING DATE: 19930622
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brotman, Harris F.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-3630
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 936 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-05944-2
;
; Query Match 67.3%; Score 37; DB 5; Length 936;
; Best Local Similarity 71.4%; Pred. No. 2e+02;
; Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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; QY 3 FKDWEEL 9
; DB 3 FKDWEEL 9

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Db 551 FKDWDEM 557

RESULT 15
US-09-308-453-2
; Sequence 2, Application US/09308453
; Patent No. 6475764
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GMBH
; TITLE OF INVENTION: Recombinant collagenase type I from Clostridium histolyticum and
; TITLE OF INVENTION: for isolating cells and groups of cells
; FILE REFERENCE: BMID9924US
; CURRENT APPLICATION NUMBER: US/09/308,453
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 1008
; TYPE: PRT
; ORGANISM: Clostridium histolyticum
US-09-308-453-2

Query Match 67.3%; Score 37; DB 4; Length 1008;
Best Local Similarity 71.4%; Pred.No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

2y 3 FKDWDEL 9
Db 623 FKDWDEM 629

Search completed: December 23, 2003, 08:53:50
Job time : 10.6 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	55	100.0	9	10	US-09-989-621-4	Sequence 4, Appli
2	52	94.5	154	15	US-10-209-264-5	Sequence 5, Appli
3	43	78.2	1145	9	US-09-815-242-11211	Sequence 11211, A
4	36	65.5	283	9	US-09-935-339-984	Sequence 984, App
5	36	65.5	283	11	US-09-525-293-984	Sequence 984, App
6	36	65.5	316	12	US-09-907-218-76	Sequence 76, Appl
7	36	65.5	316	12	US-10-387-623-120	Sequence 120, App
8	36	65.5	620	15	US-10-156-761-14439	Sequence 14439, A
9	35	63.6	26	11	US-09-984-245-150	Sequence 150, App
10	35	63.6	26	11	US-09-966-260-150	Sequence 150, App
11	35	63.6	26	11	US-09-983-965-150	Sequence 150, App
12	35	63.6	26	15	US-10-143-090-150	Sequence 150, App
13	35	63.6	107	9	US-09-864-761-43456	Sequence 43456, A
14	34.5	62.7	84	12	US-10-340-578-57	Sequence 57, Appl
15	34	61.8	219	12	US-10-223-081-332	Sequence 332, App

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US-10-209-264-5
; Sequence 5, Application US/10209264
; Publication No. US2003003111A1
; GENERAL INFORMATION:
; APPLICANT: Con, Chong Jin
;           Lim, Gek Keow
;           Zhao, Yi
;           Chen, Wei Ning
; TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
;                   USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Ladas & Parry
;             STREET: 26 West 61 Street
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/209,264
; FILING DATE: 31-Jul-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/SG98/00046
; FILING DATE: 19-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maes, Clifford J.
; REGISTRATION NUMBER: 30,086
; REFERENCE/DOCKET NUMBER: U-013109-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 154 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-209-264-5
Query Match          94.5%; Score 52; DB 15; Length 154;
Best Local Similarity 88.9%; Pred. No. 0.38;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CLFKDWEEL 9
Db      115 CVFKDWEEL 123

RESULT 3
US-09-815-242-11211
; Sequence 11211, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078

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; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11211
; LENGTH: 1146
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-815-242-11211
Query Match          78.2%; Score 43; DB 9; Length 1146;
Best Local Similarity 77.8%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CLFKDWEEL 9
Db      69 CLFPDWETL 77

RESULT 4
US-09-925-299-984
; Sequence 984, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 984
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (103)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (268)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-984
Query Match          65.5%; Score 36; DB 9; Length 283;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CLFKDWE 7
Db      114 CLFKDWE 120

RESULT 5
US-09-925-299-984
; Sequence 984, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:

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; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA102
 ; CURRENT APPLICATION NUMBER: US/09/925,299
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05893
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1556
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 984
 ; LENGTH: 283
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (103)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (268)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; US-09-925-299-984

Query Match 65.5%; Score 36; DB 11; Length 283;
 Best Local Similarity 71.4%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLFKDWE 7
 DB 114 CFLKDWE 120

RESULT 6
 US-09-907-218-76
 ; Sequence 76, Application US/09907218
 ; Publication No. US20030168645A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Mishra, Vishnu
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Tailon, Bruce
 ; APPLICANT: Casman, Stacie J
 ; APPLICANT: Wolenc, Adam Ryan
 ; APPLICANT: Li, Li
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Spytek, Kimberly Ann
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 21402-061
 ; CURRENT APPLICATION NUMBER: US/09/907,218
 ; PRIOR FILING DATE: 2002-04-04
 ; PRIOR APPLICATION NUMBER: 60/218,746
 ; PRIOR FILING DATE: 2000-07-17
 ; PRIOR APPLICATION NUMBER: 60/260,977
 ; PRIOR FILING DATE: 2001-01-11
 ; PRIOR APPLICATION NUMBER: 60/263,801
 ; PRIOR FILING DATE: 2001-01-24
 ; PRIOR APPLICATION NUMBER: 60/268,226
 ; PRIOR FILING DATE: 2001-02-12
 ; PRIOR APPLICATION NUMBER: 60/271,622
 ; PRIOR FILING DATE: 2001-02-26
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 76
 ; LENGTH: 316
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-907-218-76

Query Match 65.5%; Score 36; DB 12; Length 316;
 Best Local Similarity 71.4%; Pred. No. 3.1e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFKDWE 8
 DB 308 LFKDWE 314

RESULT 7
 US-10-387-629-120
 ; Sequence 120, Application US/10387629
 ; Publication No. US20030221205A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ChemCom S.A.
 ; APPLICANT: Veithen, Alex
 ; TITLE OF INVENTION: Olfactory and Pheromones G-Protein coupled Receptors
 ; FILE REFERENCE: 9409/2192
 ; CURRENT APPLICATION NUMBER: US/10/387,629
 ; CURRENT FILING DATE: 2003-03-13
 ; NUMBER OF SEQ ID NOS: 254
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 120
 ; LENGTH: 316
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; US-10-387-629-120

Query Match 65.5%; Score 36; DB 12; Length 316;
 Best Local Similarity 71.4%; Pred. No. 3.1e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFKDWE 8
 DB 308 LFKDWE 314

RESULT 8
 US-10-156-761-14439
 ; Sequence 14439, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; CURRENT FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 14439
 ; LENGTH: 620
 ; TYPE: PRT
 ; ORGANISM: Streptomyces avermitilis
 ; US-10-156-761-14439

Query Match 65.5%; Score 36; DB 15; Length 620;
 Best Local Similarity 75.0%; Pred. No. 5.9e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFKDWE 9
 DB 147 LFKDWE 154

RESULT 9
 US-09-984-245-150
 ; Sequence 150, Application US/09984245
 ; Patent No. US20020165374A1

GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/984,245
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
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; PRIOR FILING DATE: 1997-05-30
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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
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; PRIOR APPLICATION NUMBER: US 60/048,096
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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 150
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-245-150

Query Match 63.6%; Score 35; DB 10; Length 26;
Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 LFKDWEL 9
Db 4 IFKEWENL 11

RESULT 10
US-09-966-262-150
; Sequence 150, Application US/09966262
; Publication No. US20030050461A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/966,262
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: US 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 150
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-262-150

Query Match 63.6%; Score 35; DB 11; Length 26;

Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFKDWEEL 9
Db 4 IFKEWENL 11

RESULT 11
US-09-983-966-150
; Sequence 150, Application US/09983966
; Publication No. US20030060619A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/983,966
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
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; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
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; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 150

; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-966-150

Query Match 63.6%; Score 35; DB 11; Length 26;
Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFKDWEEL 9
Db 4 IFKEWENL 11

RESULT 12
US-10-143-090-150
; Sequence 150, Application US/10143090
; Publication No. US20030069406A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/10/143,090
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 150
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-143-090-150

Query Match 63.6%; Score 35; DB 15; Length 26;
Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFKDWEEL 9
Db 4 IFKEWENL 11

RESULT 13
US-09-864-761-43456
; Sequence 43456, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Weisheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43456
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004682.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EST HUMAN HIT: BF182859.1, EVALUATE 1.00e-34
; OTHER INFORMATION: SWISSPROT HIT: Q92620, EVALUATE 1.00e-35
US-09-864-761-43456

```

```

Query Match      63.6%; Score 35; DB 9; Length 107;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      3 PKDWE 8
Db      79 YKDWE 84

```

```

RESULT 14
US-10-340-578-57
; Sequence 57, Application US/10340578
; Publication No. US20030153097A1
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: DESHAIES, Raymond J.
; APPLICANT: COPE, Gregory
; APPLICANT: VERMA, Rati
; APPLICANT: AMBROGGIO, Xavier J.
; TITLE OF INVENTION: MODULATION OF COP9 SIGNALSOME ISOPEPTIDASE ACTIVITY
; FILE REFERENCE: CIT1590-1.
; CURRENT APPLICATION NUMBER: US/10/340,578
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 60/355,334
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 10/047,253
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 10/046,961
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/261,314
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/322,322
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US 60/322,030
; PRIOR FILING DATE: 2001-09-14

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; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Ralstonia solanacearum
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (41)..(41)
; OTHER INFORMATION: Xaa indicates 18 amino acid residues
US-10-340-578-57

Query Match      62.7%; Score 34.5; DB 12; Length 84;
Best Local Similarity 50.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

Qy      1 CLFKD-----WEEL 9
Db      23 CLFLDYRHRLIAWEEL 38

RESULT 15
US-10-223-081-332
; Sequence 332, Application US/10223081
; Publication No. US2003018686A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe P.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PIC7
; CURRENT APPLICATION NUMBER: US/10/223,081
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 332
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-081-332

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Query Match 61.8%; Score 34; DB 12; Length 219;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Cy 2 LFXDWHEEL 9
Db 126 LFKWQDM 133

Search completed: December 23, 2003, 08:52:50
Job time : 80.4 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 11 Seconds
(without alignments)
78.683 Million cell updates/sec

Title: US-09-989-621-4

Perfect score: 55

Sequence: 1 CLFKDWEEL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	134	1 B48345	gene X protein, tr
2	55	100.0	154	1 QOVL1	gene X protein - h
3	55	100.0	154	1 QOVL1	gene X protein - h
4	55	100.0	154	1 QOVL1	gene X protein - h
5	55	100.0	154	1 A48345	gene X protein - h
6	55	100.0	154	2 S47404	gene X protein - h
7	55	100.0	154	2 S31300	gene X protein - h
8	55	100.0	154	2 S35529	gene X protein - h
9	55	100.0	154	2 T13466	gene X protein - h
10	55	100.0	210	2 S12598	gene X protein - h
11	52	94.5	154	1 QOVL1	gene X protein - h
12	52	94.5	154	1 QOVL1	gene X protein - h
13	52	94.5	154	1 QOVL1	gene X protein - h
14	52	94.5	154	2 S20756	gene X protein - h
15	52	94.5	154	2 S47408	gene X protein - h
16	52	94.5	154	2 J02228	trans-activating p
17	52	94.5	154	2 S25650	gene X protein - h
18	52	94.5	154	2 S3687	gene X protein - h
19	52	94.5	154	2 S2542	gene X protein - h
20	52	94.5	154	2 S20751	gene X protein - h
21	52	94.5	172	2 A58456	gene X protein - h
22	52	94.5	359	2 S04570	gene X/C fusion pr
23	51	92.7	154	1 QOVL1	gene X protein - h
24	51	92.7	154	2 S23119	gene X protein - h
25	51	92.7	210	2 T13472	gene X protein - h
26	48	87.3	154	2 S67503	gene X protein - h
27	43	78.2	154	2 S0256	gene X protein - h
28	43	78.2	154	2 J80603	gene X protein - h
29	43	78.2	1146	1 I64112	transcription/rep

30 42 76.4 154 2 JS0604 gene X protein - h
31 42 76.4 715 2 B71073 hypothetical prote
32 40 72.7 453 2 A89373 hypothetical prote
33 39 70.9 601 2 C81414 penicillin-binding
34 38 69.1 242 2 S49489 trypsin (EC 3.4.21
35 38 69.1 736 2 D90574 hypothetical prote
36 37 67.3 123 2 B86296 T24D18.25 protein
37 37 67.3 230 2 H97331 response regulator
38 37 67.3 260 2 A12481 hypothetical prote
39 37 67.3 344 2 A81884 probable phage pro
40 37 67.3 385 2 S49111 peptide synthetase
41 37 67.3 398 2 G72333 conserved hypothet
42 37 67.3 715 2 B75135 DNA helicase relat
43 37 67.3 1271 2 T43269 microcystin synthet
44 37 67.3 1539 2 T30037 hypothetical prote
45 37 67.3 1756 2 T07566 hypothetical prote

ALIGNMENTS

RESULT 1

B48345 gene X protein, truncated form - hepatitis B virus

C/Species: hepatitis B virus, HBV

C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999

C/Accession: B48345

R/Repp, R.; Keller, C.; Borkhardt, A.; Csecke, A.; Schaefer, S.; Gerlich, W.H.; Lampert, Arch. Virol. 125, 299-304, 1992

A/Title: Detection of a hepatitis B virus variant with a truncated X gene and enhancer I

A/Reference number: A48345; MUID:92352333; PMID:1642555

A/Accession: B48345

A/Molecule type: DNA

A/Residues: 1-134 <REP>

A/Cross-references: GB:S41176; NID:9252541; PIDN:AAB22733.1; PID:3252542

A/Note: sequence extracted from NCBI backbone (NCBIN:109914, NCBIP:109915)

C/Genetics:

A/Gene: X

C/Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 55; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9

DB 115 CLFKDWEEL 123

RESULT 2

QOVL1 gene X protein - hepatitis B virus (subtype ayw)

C/Species: hepatitis B virus, HBV

C/Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 08-Apr-1994

C/Accession: A03719

R/Galibert, F.; Mandart, E.; Fitoussi, F.; Tiollais, P.; Charnay, P.

A/Title: Nucleotide sequence of the hepatitis B virus genome (subtype ayw) in E. coli.

A/Reference number: A93214; MUID:81012891; PMID:399327

A/Accession: A03719

A/Molecule type: DNA

A/Residues: 1-154 <GAL>

A/Cross-references: GB:J02203; GB:V01460

C/Genetics:

A/Gene: X

C/Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 55; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9

DB 115 CLFKDWEEL 123

```

Db      115 CLFKDWEEL 123

RESULT 3
QQVLEH
Gene X protein - hepatitis B virus (subtype ayw, strain PHB320)
C/Species: hepatitis B virus, HBV
A/Variety: subtype ayw, strain PHB320
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Jul-2000
C/Accession: A05237; S53144; S53173; S53195; S53210; S53222; S53224; S53235; S53280
R:Bichko, V.; Pushko, P.; Dreilina, D.; Pumpen, P.; Gren, E.
FEBS Lett. 185, 208-212, 1985
A/Title: Subtype ayw variant of hepatitis B virus: DNA primary structure analysis.
A/Reference number: A05237; MUID:85204397; PMID:3996597
A/Accession: A05237
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-154 <BIG>
A/Cross-references: EMBL:X02496; NID:G62280; PIDN:CAB41697.1; PID:G4704317
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A/Reference number: S53112
A/Accession: S53144
A/Molecule type: DNA
A/Residues: 124-154 <LAI>
A/Cross-references: EMBL:X85267; NID:G736025; PIDN:CAA59548.1; PID:G736026; EMBL:X85284;
S5305; EMBL:X83307; EMBL:X83308; EMBL:X85310; EMBL:X85312; EMBL:X85315; EMBL:
A/Experimental source: isolate patient Pintus'85 et al.
A/Accession: S53173
A/Molecule type: DNA
A/Residues: 124-154 <LA2>
A/Cross-references: EMBL:X85277; NID:G736065; PIDN:CAA59575.1; PID:G736066
A/Experimental source: isolate patient Bio'90
C/Genetics:
A/Gene: X
C/Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 55; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CLFKDWEEL 9
      |||||
Db      115 CLFKDWEEL 123

RESULT 4
A48345
Gene X protein - hepatitis B virus
C/Species: hepatitis B virus, HBV
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C/Accession: A48345
R:Repp, R.; Keller, C.; Borkhardt, A.; Ceecke, A.; Schaefer, S.; Gerlich, W.H.; Lampert,
Arch. Virol. 125, 299-304, 1992
A/Title: Detection of a hepatitis B virus variant with a truncated X gene and enhancer I
A/Reference number: A48345; MUID:92352333; PMID:1642555
A/Accession: A48345
A/Molecule type: DNA
A/Residues: 1-154 <REP>
A/Cross-references: GB:S41175; NID:G252539; PIDN:ABA2732.1; PID:G252540
A/Note: sequence extracted from NCBI backbone (NCBIN:109912, NCBIPI:109913)
C/Genetics:
A/Gene: X
C/Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 55; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CLFKDWEEL 9
      |||||
Db      115 CLFKDWEEL 123

RESULT 5
S47404
Gene X protein - hepatitis B virus (subtype ayw4)
C/Species: hepatitis B virus, HBV
A/Variety: subtype ayw4
C/Date: 23-Nov-1994 #sequence_revision 12-May-1995 #text_change 26-Aug-1999
C/Accession: S47404
R:Plucienniczak, A.
submitted to the EMBL Data Library, August 1994
A/Description: Molecular cloning and sequencing of two complete genomes of polish isola
A/Reference number: S47404
A/Accession: S47404
A/Molecule type: DNA
A/Residues: 1-154 <PLU>
A/Cross-references: EMBL:Z35716; NID:G527435; PIDN:CAA84785.1; PID:G527436
A/Experimental source: subtype ayw4
C/Genetics:
A/Gene: X
C/Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 55; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CLFKDWEEL 9
      |||||
Db      115 CLFKDWEEL 123

RESULT 6
S53130
Gene X protein - hepatitis B virus
C/Species: hepatitis B virus, HBV
C/Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C/Accession: S53130
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A/Reference number: S53112
A/Accession: S53130
A/Molecule type: DNA
A/Residues: 1-154 <LAI>
A/Cross-references: EMBL:X85254; NID:G736003; PIDN:CAA59513.1; PID:G736007
C/Genetics:
A/Gene: X
C/Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 55; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CLFKDWEEL 9
      |||||
Db      115 CLFKDWEEL 123

RESULT 7
S35529
Gene X protein - hepatitis B virus (subtype adr)
C/Species: hepatitis B virus, HBV
A/Variety: subtype adr
C/Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C/Accession: S35529
R:Mukaide, M.; Kumazawa, T.; Hoehi, A.; Kawaguchi, R.; Hiki, K.
Nucleic Acids Res. 20, 6105, 1992
A/Title: The complete nucleotide sequence of hepatitis B virus, subtype adr (SRADR) and
A/Reference number: S35527; MUID:93096607; PMID:11461746
A/Accession: S35529
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-154 <MUK>

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A;Cross-references: EMBL:D12980; NID:g221500; PIDN:BAA02356.1; PID:g221503
A;Experimental source: subtype adr
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 55; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
| | | | |
Db 115 CLFKDWEEL 123

RESULT 8
S32203
gene X protein - hepatitis B virus (subtype ayw, patient C1000)
C;Species: hepatitis B virus, HBV
A;Variety: subtype ayw, patient C1000
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C;Accession: S32203
R;Pretzler-Adams, S.; Schlager, M.J.; Peters, T.; Hettler, F.; Gerok, W.; Rasenack, J.
submitted to the EMBL Data Library, March 1993
A;Description: Identification and sequence analysis of hepatitis B virus DNA in immunol
A;Reference number: S32202
A;Accession: S32203
A;Molecule type: DNA
A;Residues: 1-154 <PRE>
A;Cross-references: EMBL:X72702; NID:g288927; PIDN:CAAS1256.1; PID:g288929
A;Experimental source: subtype ayw, patient C1000
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 55; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
| | | | |
Db 115 CLFKDWEEL 123

RESULT 9
T13466
gene X protein - hepatitis B virus (isolate 09D09HCC)
C;Species: hepatitis B virus, HBV
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
C;Accession: T13466
R;Takahashi, K.; Akahane, Y.; Hino, K.; Ohta, Y.; Mishi, S.
Arch Virol. 143, 2313-2326, 1998
A;Title: Hepatitis B virus genomic sequence in the circulation of hepatocellular carcin
A;Reference number: Z17684; MUID:99129050; PMID:9930189
A;Accession: T13466
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-154 <TAK>
A;Cross-references: EMBL:AB014368; NID:g3551304; PIDN:BAA32861.2; PID:g6116706
A;Experimental source: Japanese patient with hepatocellular carcinoma isolate 09D09HCC
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 55; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
| | | | |
Db 115 CLFKDWEEL 123

RESULT 10

S12598
gene X protein - hepatitis B virus (subtype adr)
N;Contains: pre-X domain
C;Species: hepatitis B virus, HBV
A;Variety: subtype adr
C;Date: 13-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jan-2000
R;Loncarevic, I.F.; Zentgraf, H.; Schroeder, C.H.
Nucleic Acids Res. 18, 4940, 1990
A;Title: Sequence of a replication competent hepatitis B virus genome with a preX open ;
A;Reference number: S12598; MUID:90370503; PMID:2395664
A;Accession: S12598
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-210 <LON>
A;Cross-references: EMBL:X52939
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 55; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
| | | | |
Db 171 CLFKDWEEL 179

RESULT 11
QQVLAW
gene X protein - hepatitis B virus (subtype adw and adw2)
C;Species: hepatitis B virus, HBV
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 30-Jun-1998
C;Accession: A31289; B94409; A03719
R;Lo, S.J.; Chien, M.L.; Lee, Y.H.W.
Virology 167, 289-292, 1988
A;Title: Characteristics of the X gene of hepatitis B virus.
A;Reference number: A31289; MUID:89045656; PMID:3188399
A;Accession: A31289
A;Molecule type: DNA
A;Residues: 1-154 <LOS>
A;Experimental source: subtype adw
R;Valenzuela, P.; Quiroga, M.; Zaldivar, J.; Gray, P.; Rutter, W.J.
in Animal Virus Genetics, Field, B.N., Jaenisch, R., and Fox, C.F., eds., pp.57-70, Acad
A;Reference number: A94409
A;Accession: B94409
A;Molecule type: DNA
A;Residues: 1-154 <VAL>
A;Experimental source: subtype adw2
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match 94.5%; Score 52; DB 1; Length 154;
Best Local Similarity 88.9%; Pred. No. 0.056;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
| | | | |
Db 115 CVFKDWEEL 123

RESULT 12
QQVLKS
gene X protein - hepatitis B virus (subtype adw, strain 991)
C;Species: hepatitis B virus, HBV
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: S10380
R;Koechel, H.G.; Schueler, A.; Lottmann, S.; Thomssen, R.
submitted to the EMBL Data Library, February 1990

A;Reference number: S10380
 A;Accession: S10380
 A;Molecule type: DNA
 A;Residues: 1-154 <KOE>
 A;Cross-references: EMBL:X51970; NID:G1155012; PIDN:CRA36231.1; PID:G60432
 C;Genetics:
 A;Gene: X
 C;Superfamily: hepatitis B virus gene X protein

Query Match 94.5%; Score 52; DB 1; Length 154;
 Best Local Similarity 88.9%; Pred. No. 0.056;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLFKDWEEL 9
 :|||||
 Db 115 CVFKDWEEL 123

RESULT 13

QOVLCP
 Gene X protein - hepatitis B virus (strain LSH, chimpanzee)
 C;Species: hepatitis B virus, HBV
 C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jun-2000
 C;Accession: D28885
 R;Vaudin, M.; Wolstenholme, A.J.; Tsiquaye, K.N.; Zuckerman, A.J.; Harrison, T.J.
 J. Gen. Virol. 69, 1383-1389, 1988
 A;Title: The complete nucleotide sequence of the genome of a hepatitis B virus isolated
 A;Reference number: A92796; MUID:88258473; PMID:2838576
 A;Accession: D28885
 A;Molecule type: DNA
 A;Residues: 1-154 <VAU>
 A;Cross-references: GB:D00220; NID:G221505; PIDN:BAA00160.1; PID:G221509
 C;Genetics:
 A;Gene: X
 C;Superfamily: hepatitis B virus gene X protein

Query Match 94.5%; Score 52; DB 1; Length 154;
 Best Local Similarity 88.9%; Pred. No. 0.056;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLFKDWEEL 9
 :|||||
 Db 115 CVFKDWEEL 123

RESULT 14

S20756
 Gene X protein - hepatitis B virus (subtype ayw, patient E)
 C;Species: hepatitis B virus, HBV
 A;Variety: subtype ayw, patient E
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C;Accession: S20756
 R;Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Melis, A.; Porru, A.
 submitted to the EMBL Data Library, March 1992
 A;Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negative
 A;Reference number: S20745
 A;Accession: S20756
 A;Molecule type: DNA
 A;Residues: 1-154 <LAI>
 A;Cross-references: EMBL:X65259; NID:G59439; PIDN:CRA46360.1; PID:G59443
 A;Experimental source: subtype ayw, patient E
 C;Genetics:
 A;Gene: X
 C;Superfamily: hepatitis B virus gene X protein

Query Match 94.5%; Score 52; DB 2; Length 154;
 Best Local Similarity 88.9%; Pred. No. 0.056;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLFKDWEEL 9
 :|||||
 Db 115 CVFKDWEEL 123

RESULT 15

S47408
 Gene X protein - hepatitis B virus (subtype adw2)
 C;Species: hepatitis B virus, HBV
 A;Variety: subtype adw2
 C;Date: 23-Nov-1994 #sequence_revision 12-May-1995 #text_change 26-Aug-1999
 C;Accession: S47408
 R;Plucieniczak, A.
 submitted to the EMBL Data Library, August 1994
 A;Description: Molecular cloning and sequencing of two complete genomes of polish isola
 A;Reference number: S47404
 A;Accession: S47408
 A;Molecule type: DNA
 A;Residues: 1-154 <PLU>
 A;Cross-references: EMBL:Z35717; NID:G527440; PIDN:CRA84789.1; PID:G527441
 A;Experimental source: subtype adw2
 C;Genetics:
 A;Gene: X
 C;Superfamily: hepatitis B virus gene X protein

Query Match 94.5%; Score 52; DB 2; Length 154;
 Best Local Similarity 88.9%; Pred. No. 0.056;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLFKDWEEL 9
 :|||||
 Db 115 CVFKDWEEL 123

Search completed: December 23, 2003, 08:41:09
 Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 6.4 Seconds
(without alignments) updates/sec
66.131 Million cell

Title: US-09-989-621-4
Perfect score: 55
Sequence: 1 CLFKDWEEL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	154	1 X_HPBV4	P12936 hepatitis b
2	55	100.0	154	1 X_HPBV4	P03165 hepatitis b
3	52	94.5	154	1 X_HPBV2	P03165 hepatitis b
4	52	94.5	154	1 X_HPBV2	P17102 hepatitis b
5	52	94.5	154	1 X_HPBV4	P12912 hepatitis b
6	52	94.5	154	1 X_HPBV4	Q05499 hepatitis b
7	51	92.7	154	1 X_HPBV4	P24026 hepatitis b
8	43	78.2	154	1 X_HPBV4	P20977 hepatitis b
9	43	78.2	154	1 X_HPBV4	P20977 hepatitis b
10	43	78.2	154	1 X_HPBV4	P45128 haemophilus
11	42	76.4	154	1 X_HPBV4	P20975 hepatitis b
12	42	76.4	154	1 X_HPBV4	O59025 pyrococcus
13	38	69.1	1023	1 DPOI_ADEB3	O72540 bovine aden
14	37	67.3	1715	1 HELS_PIRAB	Q9V049 pyrococcus
15	37	67.3	1756	1 YCFI_PINTH	P41647 pinus thunb
16	36	65.5	316	1 YCFI_PINTH	Q9UGF7 homo sapien
17	36	65.5	347	1 VIPL_MOUSE	P59481 mus musculu
18	36	65.5	354	1 AROC_BUCAI	P57198 buchnera ap
19	36	65.5	356	1 VP36_CANFA	P49256 canis famil
20	36	65.5	356	1 VP36_HUMAN	Q12907 homo sapien
21	36	65.5	358	1 VP36_MOUSE	Q9DBH5 mus musculu
22	36	65.5	607	1 PRIM_MYCCE	P47492 mycoplasma
23	36	65.5	620	1 PRIM_MYCCE	P74932 mycoplasma
24	36	65.5	704	1 HELS_SULTO	Q97481 sulfolobus
25	35	63.6	311	1 FNPH_YEAST	Q05788 saccharomyc
26	35	63.6	353	1 AROC_BUCAP	Q9ZHE9 buchnera ap
27	35	63.6	413	1 YGSO_YEAST	P45819 saccharomyc
28	35	63.6	484	1 AMYA_ASPNG	P56271 aspergillus
29	35	63.6	662	1 HEPA_HSV6U	P52375 human herpe
30	35	63.6	662	1 HEPA_HSV6Z	P52451 human herpe
31	35	63.6	708	1 GUNL_SULSO	Q97W99 sulfolobus
32	35	63.6	879	1 GUNL_CLOTID	Q02934 clostridium
33	35	63.6	880	1 YVL7_CABEL	Q21534 caenorhabdi

RESULT 1

X_HPBV4
ID X_HPBV4
AC P12936; STANDARD; PRT; 154 AA.
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adr4).
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10409;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83246570; PubMed=6306594;
RA Fujiyama A., Miyanochara A., Nozaki C., Yoneyama T., Ohtomo N.,
RA Matsubara K.,
RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype
RT adr";
RL Nucleic Acids Res. 11:4601-4610(1983).
CC - FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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CC
CC EMBL; X01587; CAA25744.1; -
CC InterPro; IPR000236; TransactX.
CC Pfam; PF00739; X; 1.
CC SEQUENCE 154 AA; 16622 MW; 594A1D0716928804 CRC64;
Query Match 100.0%; Score 55; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.0052; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0

RESULT 2

X_HPBV4
ID X_HPBV4
AC P03165; STANDARD; PRT; 154 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype ayw).
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10418;
QY 1 CLFKDWEEL 9
DB 115 CLFKDWEEL 123
Query Match 100.0%; Score 55; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.0052; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0

```

RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=81012091; PubMed=399327;
RA  Galibert F., Mandart E., Fickoussi F., Tiollais P., Charnay P.;
RT  "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)
RL  cloned in E. coli.";
RL  Nature 281:646-650(1979).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  STRAIN=Latvia;
RX  MEDLINE=85204397; PubMed=3995597;
RA  Bichko V., Drailina D., Puskho P.M., Pumpen P.P., Gren E.;
RT  "Subtype ayw variant of hepatitis B virus. DNA primary structure
RT  analysis.";
RL  FEBS Lett. 185:208-212(1985).
RN  [3]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=85204397; PubMed=3995597;
RA  Bichko V., Drailina D., Puskho P.M., Pumpen P.P., Gren E.;
RT  "Subtype ayw variant of hepatitis B virus. DNA primary structure
RT  analysis.";
RL  FEBS Lett. 185:208-212(1985).
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CC  -----
DR  EMBL; V01460; -; NOT_ANNOTATED_CDS.
DR  EMBL; X02496; CAB41697.1; -.
DR  PIR; A03719; QOVLDI1.
DR  PIR; A05237; QOVLH.
DR  InterPro; IPR000236; TransactX.
DR  Pfam; PF00739; X; 1.
FT  VARIANT 46 46 P -> S (IN STRAIN LATVIA).
FT  VARIANT 84 88 NAHQI -> KQPP (IN STRAIN LATVIA).
FT  VARIANT 102 102 A -> V (IN STRAIN LATVIA).
FT  CONFLICT 26 26 R -> C (IN REF. 1).
SQ  SEQUENCE 154 AA; 16618 MW; 29FD1CC9E09A34B5 CRC64;
Query Match 100.0%; Score 55; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CLFKDWEEL 9
DB 115 CLFKDWEEL 123
X_HPBV2
ID X_HPBV2 STANDARD; PRT; 154 AA.
AC P03166; P12935;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw2), and
OS Hepatitis B virus (subtype adw).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCB1_TaxID=10408, 106821;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ADW2;
RA Valenzuela P., Quiroga M., Zaidivar J., Gray P., Rutter W.J.;
RL (In) Field B.N., Jaenisch R., Fox C.F. (eds.);
RL Animal virus genetics, pp.57-70, Academic Press, New York (1980).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=ADW;
RX MEDLINE=89045656; PubMed=3188399;
RA Lo S.J., Chien M.L., Lee Y.H.W.;
RT "Characteristics of the X gene of hepatitis B virus.";
RL Virology 167:289-292(1988).
RN [3]

```

```

RP SEQUENCE FROM N.A.
RX STRAIN=ADW;
RX MEDLINE=83168919; PubMed=6300776;
RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
RT DNA; subtype adr and adw.";
RL Nucleic Acids Res. 11:1747-1757(1983).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=ADW;
RX MEDLINE=83168919; PubMed=6300776;
RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
RT DNA; subtype adr and adw.";
RL Nucleic Acids Res. 11:1747-1757(1983).
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CC -----
DR  EMBL; X02763; CAA36540.1; -.
DR  EMBL; Z35717; CAA84789.1; -.
DR  EMBL; M23692; AAA56820.1; -.
DR  EMBL; V00866; -; NOT_ANNOTATED_CDS.
DR  PIR; A31289; QOVLAW.
DR  PIR; S47408; S47408.
DR  InterPro; IPR000236; TransactX.
DR  Pfam; PF00739; X; 1.
FT  CONFLICT 80 80 E -> A (IN REF. 3).
FT  CONFLICT 115 115 C -> S (IN REF. 2).
FT  CONFLICT 130 131 KV -> MI (IN REF. 3).
SQ  SEQUENCE 154 AA; 16593 MW; 7F2AE32A4F025670 CRC64;
Query Match 94.5%; Score 52; DB 1; Length 154;
Best Local Similarity 88.9%; Pred. No. 0.018;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CLFKDWEEL 9
DB 115 CLFKDWEEL 123
X_HPBV9
ID X_HPBV9 STANDARD; PRT; 154 AA.
AC P17102;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw / strain 991).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCB1_TaxID=10410;
RN [1]
RP SEQUENCE FROM N.A.
RX Koechel H.G., Schueler A., Lottmann S., Thomssen R.;
RL Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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CC -----
DR  EMBL; X51970; CAA36231.1; -.
DR  PIR; S10380; QOVLKS.
DR  InterPro; IPR000236; TransactX.
DR  Pfam; PF00739; X; 1.
SQ  SEQUENCE 154 AA; 16553 MW; 52A0D9CEFE6DCDE0 CRC64;
Query Match 94.5%; Score 52; DB 1; Length 154;
Best Local Similarity 88.9%; Pred. No. 0.018;

```

ID	XREFVU	STANDARD;	PRT;	154 AA.
AC	P20976;			
DT	01-FEB-1991	(Rel. 17, Created)		

J. Gen. Virol. 74:1627-1632(1993).

DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Trans-activating protein X.
 GN X.
 OS Hepatitis B virus (subtype adv / strain Japan/pJDM233).
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10413;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89010694; PubMed=3171552;
 RA Okamoto H., Tsuda F., Sakugawa H., Sastrosowignjo R.I., Imai M.,
 RA Miyakawa Y., Mayumi M.;
 RA "Typing hepatitis B virus by homology in nucleotide sequence:
 RT comparison of surface antigen subtypes.";
 RL J. Gen. Virol. 69:2575-2583(1988).
 RC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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 CC
 CC EMBL; D00329; -; NOT ANNOTATED_CDS.
 DR PIR; JS0256; JS0256.
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 SQ SEQUENCE 154 AA; 16595 MW; 512A5A077169D5CA CRC64;
 Query Match 78.2%; Score 43; DB 1; Length 154;
 Best Local Similarity 66.7%; Pred. No. 0.74;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CLFQDWEEL 9
 Db 115 CWFNEWEEL 123

RESULT 9
 X HPBVO
 ID X HPBVO STANDARD; PRT; 154 AA.
 AC P20977;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Trans-activating protein X.
 GN X.
 OS Hepatitis B virus (subtype adv / strain Okinawa/pODW282).
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10413;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89010694; PubMed=3171552;
 RA Okamoto H., Tsuda F., Sakugawa H., Sastrosowignjo R.I., Imai M.,
 RA Miyakawa Y., Mayumi M.;
 RA "Typing hepatitis B virus by homology in nucleotide sequence:
 RT comparison of surface antigen subtypes.";
 RL J. Gen. Virol. 69:2575-2583(1988).
 RC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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 CC
 CC EMBL; D00330; -; NOT ANNOTATED_CDS.
 DR PIR; JS0603; JS0603.
 DR InterPro; IPR000236; TransactX.

DR Pfam; PF00739; X; 1.
 SQ SEQUENCE 154 AA; 16558 MW; E2646C059A30125F CRC64;
 Query Match 78.2%; Score 43; DB 1; Length 154;
 Best Local Similarity 66.7%; Pred. No. 0.74;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CLFQDWEEL 9
 Db 115 CWFNEWEEL 123

RESULT 10
 X HPBVO
 ID X HPBVO STANDARD; PRT; 1146 AA.
 AC P45128;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transcription-repair coupling factor (TRCF).
 GN MFD OR H11258.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=RD / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Klevorick A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Usterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
 Rd.";
 RL Science 269:496-512(1995).
 CC -!- FUNCTION: NECESSARY FOR STRAND-SPECIFIC REPAIR. A LESION IN THE
 CC TEMPLATE STRAND BLOCKS THE RNA POLYMERASE COMPLEX (RNAP). THE
 CC RNAP-DNA-RNA COMPLEX IS SPECIFICALLY RECOGNIZED BY TRCF WHICH
 CC RELEASES RNAP AND THE TRUNCATED TRANSCRIPT; THE TRCF MAY REPLACE
 CC RNAP AT THE LESION SITE AND THEN RECRUIT THE UVRA/B/C REPAIR
 CC SYSTEM (BY SIMILARITY).
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE UVRB FAMILY.
 CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE HELICASE
 CC FAMILY. RECG SUBFAMILY.
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 CC EMBL; U32805; AAC22905.1; -
 DR PIR; I64112; I64112.
 DR TIGR; H11258; -
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR004576; Mfd.
 DR InterPro; IPR005118; TRCF.
 DR Pfam; PF02559; Card.TRCF; 1.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR Pfam; PF03461; TRCF; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELICCC; 1.
 DR TIGRFAMs; TIGR00580; mfd; 1.

KW Helicase; DNA repair; ATP-binding; DNA-binding; Complete proteome.
 FT DOMAIN 600 970 HELICASE; RECG-LIKE.
 FT NP BIND 630 637 ATP (POTENTIAL).
 FT SITE 731 734 DEEH BOX.
 SQ SEQUENCE 1146 AA; 130130 MW; 6E3052BA31978475 CRC64;

Query Match 78.2%; Score 43; DB 1; Length 1146;
 Best Local Similarity 77.8%; Pred. NO. 6.2;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLFQWHEEL 9
 ||| |||||
 Db 69 CLFQWHEEL 77

RESULT 11

X HPBVI STANDARD; PRT; 154 AA.
 ID X HPBVI
 AC P20975;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Trans-activating protein X.
 GN X.
 OS Hepatitis B virus (subtype adw / strain Indonesia/p1DW420).
 OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10412;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89010694; PubMed=3171552;
 RA Okamoto H., Tsuda F., Sakugawa H., Sastrousowigno R.I., Imai M.,
 RA Miyakawa Y., Mayumi M.;
 RT "Typing hepatitis B virus by homology in nucleotide sequence:
 RT comparison of surface antigen subtypes.";
 RL J. Gen. Virol. 69:2575-2583(1988).
 CC -1- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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 CC
 DR EMBL; D00331; -, NOT_ANNOTATED_CDS.
 DR PIR; JS0604; JS0604.
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 SQ SEQUENCE 154 AA; 16556 MW; C80C817E961BFFB9 CRC64;

Query Match 76.4%; Score 42; DB 1; Length 154;
 Best Local Similarity 66.7%; Pred. NO. 1.1;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CLFQWHEEL 9
 ||| |||||
 Db 115 CVFTWHEEL 123

RESULT 12

HEL PYRHO STANDARD; PRT; 715 AA.
 ID HELS PYRHO
 AC OS9025;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative sk12-type helicase (EC 3.6.1.1).
 GN PH1280.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=53953;

RN SEQUENCE FROM N.A.
 RP STRAIN=OT3;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudo H., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998).
 CC -1- SIMILARITY: BELONGS TO THE HELICASE FAMILY. SK12 SUBFAMILY.

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 CC
 DR EMBL; AF000005; BAA30383.1; -.
 DR PIR; E71073; E71073.
 DR HAMAP; MF_00442; -; 1.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR000445; HhH.
 DR InterPro; IPR003583; HHH_1.
 DR Pfam; PF00270; DEAD; 1.
 DR DR Pfam; PF00271; helicase_C; 1.
 DR Pfam; PF00633; HHH; 2.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELIC; 1.
 DR SMART; SM00278; HHH1; 2.
 KW Hypothetical protein; Hydrolase; Helicase; ATP-binding;
 KW Complete proteome.
 FT NP BIND 46 53 ATP (POTENTIAL).
 FT SITE 145 148 DEXH BOX.
 SQ SEQUENCE 715 AA; 82105 MW; F0E2A1AC765C999C CRC64;

Query Match 76.4%; Score 42; DB 1; Length 715;
 Best Local Similarity 100.0%; Pred. NO. 5.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FQDWHEEL 9
 ||| |||||
 Db 86 FQDWHEEL 94

RESULT 13

DPOL_ADEB3 STANDARD; PRT; 1023 AA.
 ID DPOL_ADEB3
 AC O72540;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE DNA polymerase (EC 2.7.7.7).
 GN POL.
 OS Bovine adenovirus type 3 (Mastadenovirus bos3).
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=10510;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WER-1;
 RX MEDLINE=99040086; PubMed=9820840;
 RA Yagubi A., Ojic D., Bautista D., Haj-Ahmad Y.;
 RT "Sequencing analysis of the region encoding the DNA polymerase of
 RT bovine adenovirus serotypes 2 and 3.";
 RL Intervirology 41:69-79(1998).
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 CC + {DNA}(N).

```
CC -1- MISCELLANEOUS: THIS DNA POLYMERASE REQUIRES A PROTEIN AS A PRIMER.
CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF061654; AAC16240.1; -
CC InterPro; IPR006172; DNA pol B.
CC Pfam; PF03175; DNA pol B_2; 1.
CC SMART; SM00486; POLBc_1.
CC PROSITE; PS00116; DNA_POLYMERASE_B; 1.
CC Transferrase; DNA-directed DNA polymerase; DNA replication;
CC DNA-binding.
CC SEQUENCE 1023 AA; 117728 MW; 193998701764957A CRC64;
CC
CC Query Match 69.1%; Score 38; DB 1; Length 1023;
CC Best Local Similarity 100.08; Pred. No. 43;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 3 FKDWEE 8
CC DB 294 FKDWEE 299
CC
CC RESULT 14
CC HELS_PYPAB
CC ID - HELS_PYPAB STANDARD; PRT; 715 AA.
CC AC Q9V0A9;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC DE Purative ski2-type helicase (EC 3.6.1.1.-).
CC GN PYRAB08810 OR PAB0592.
CC OS Pyrococcus abyssi.
CC OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
CC PYROCOCUS.
CC NCBI_TaxID=29292;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=GR5 / Orsay;
CC PubMed=12622808;
CC RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
CC Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
CC Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
CC "An integrated analysis of the genome of the hyperthermophilic
CC archaean Pyrococcus abyssi.";
CC Mol. Microbiol. 47:1495-1512(2003).
CC -1- SIMILARITY: BELONGS TO THE HELICASE FAMILY. SKI2 SUBFAMILY.
CC
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CC
CC EMBL; AJ248285; CAB49795.1; -
CC PIR; B75135; B75135.
CC HAMAP; MF 00442; 1.
CC InterPro; IPR001410; DEAD.
CC InterPro; IPR001650; Helicase_C.
CC InterPro; IPR000445; Hhh.
CC Pfam; PF00270; DEAD_1.
CC Pfam; PF00271; helicase_C; 1.
CC Pfam; PF00633; HHH; 2.
```

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DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR SMART; SM00278; HHH1; 2.
KW Hypothetical protein; Hydrolase; Helicase; ATP-binding;
Complete proteome.
FT NF_BIND 46 53 ATP (POTENTIAL).
FT SITE 145 148 DEXH BOX.
SQ SEQUENCE 715 AA; 82005 MW; 611401E623690EF4 CRC64;
CC
CC Query Match 67.3%; Score 37; DB 1; Length 715;
CC Best Local Similarity 85.7%; Pred. No. 45;
CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC
CC QY 3 FKDWEE 9
CC DB 88 FKDWEE 94
CC
CC RESULT 15
CC YCF1_PINTH
CC ID YCF1_PINTH STANDARD; PRT; 1756 AA.
CC AC P41647;
CC DT 01-NOV-1995 (Rel. 32, Created)
CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Hypothetical 205.3 kDa protein ycf1 (ORF 1756).
CC GN YCF1.
CC OS Pinus thunbergii (Green pine) (Japanese black pine).
CC OG Chloroplast.
CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
CC NCBI_TaxID=3350;
CC [1]
CC SEQUENCE FROM N.A.
CC MEDLINE=95024047; PubMed=7937893;
CC RA Wakasugi T., Tsudzuki J., Ito S., Nakashima K., Tsudzuki T.,
CC Sugura M.;
CC "Loss of all ndh genes as determined by sequencing the entire
CC chloroplast genome of the black pine Pinus thunbergii.";
CC Proc. Natl. Acad. Sci. U.S.A. 91:9794-9798(1994).
CC -1- FUNCTION: NOT YET KNOWN.
CC -1- SIMILARITY: BELONGS TO THE YCF1 FAMILY.
CC
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CC
CC EMBL; D17510; BAA04442.1; -
CC PIR; T07566; T07566.
CC Chloroplast; Hypothetical protein.
CC SEQUENCE 1756 AA; 205320 MW; 15C9946A8E8E7B56 CRC64;
CC
CC Query Match 67.3%; Score 37; DB 1; Length 1756;
CC Best Local Similarity 71.4%; Pred. No. 1.2e+02;
CC Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 3 FKDWEE 9
CC DB 849 FKDWEE 855
CC
CC Search completed: December 23, 2003, 08:41:52
CC Job time : 8.4 secs
```

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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:58 ; Search time 23.6 Seconds
(without alignments)
98.410 Million cell updates/sec

Title: US-09-989-621-4

Perfect score: 55

Sequence: 1 CLFKDWEEL 9

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:

- 1: sp_archaea:
- 2: sp_bacteria:
- 3: sp_fungi:
- 4: sp_human:
- 5: sp_invertebrate:
- 6: sp_mammal:
- 7: sp_mnc:
- 8: sp_organelle:
- 9: sp_phase:
- 10: sp_plant:
- 11: sp_rodent:
- 12: sp_virus:
- 13: sp_vertebrate:
- 14: sp_unclassified:
- 15: sp_virus:
- 16: sp_bacteriap:
- 17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	58	12	Q9E0S8 hepatitis b
2	55	100.0	58	12	Q9E0Q4 hepatitis b
3	55	100.0	58	12	Q9E0P6 hepatitis b
4	55	100.0	58	12	Q9E0U2 hepatitis b
5	55	100.0	58	12	Q9E0W2 hepatitis b
6	55	100.0	58	12	Q9E0S4 hepatitis b
7	55	100.0	58	12	Q9E0P2 hepatitis b
8	55	100.0	58	12	Q9E0S6 hepatitis b
9	55	100.0	58	12	Q9E0U0 hepatitis b
10	55	100.0	58	12	Q9E0Q2 hepatitis b
11	55	100.0	58	12	Q9E0N3 hepatitis b
12	55	100.0	58	12	Q9E0S2 hepatitis b
13	55	100.0	58	12	Q9E0W6 hepatitis b
14	55	100.0	58	12	Q9E0R4 hepatitis b
15	55	100.0	58	12	Q9E0W8 hepatitis b
16	55	100.0	58	12	Q9E0T4 hepatitis b

17	55	100.0	58	12	Q9E0P0	Q9E0P0 hepatitis b
18	55	100.0	58	12	Q9E0V2	Q9E0V2 hepatitis b
19	55	100.0	58	12	Q9E0U8	Q9E0U8 hepatitis b
20	55	100.0	58	12	Q9E0V4	Q9E0V4 hepatitis b
21	55	100.0	58	12	Q9E0W0	Q9E0W0 hepatitis b
22	55	100.0	58	12	Q9E0U4	Q9E0U4 hepatitis b
23	55	100.0	58	12	Q9E0T0	Q9E0T0 hepatitis b
24	55	100.0	58	12	Q9E0N6	Q9E0N6 hepatitis b
25	55	100.0	58	12	Q9E0V6	Q9E0V6 hepatitis b
26	55	100.0	58	12	Q9E0P4	Q9E0P4 hepatitis b
27	55	100.0	58	12	Q9E0T2	Q9E0T2 hepatitis b
28	55	100.0	58	12	Q9E0R8	Q9E0R8 hepatitis b
29	55	100.0	58	12	Q9E0P8	Q9E0P8 hepatitis b
30	55	100.0	58	12	Q9E0R0	Q9E0R0 hepatitis b
31	55	100.0	58	12	Q9E0R2	Q9E0R2 hepatitis b
32	55	100.0	58	12	Q9E0V0	Q9E0V0 hepatitis b
33	55	100.0	58	12	Q9E0Q8	Q9E0Q8 hepatitis b
34	55	100.0	58	12	Q9E0T6	Q9E0T6 hepatitis b
35	55	100.0	58	12	Q9E0N8	Q9E0N8 hepatitis b
36	55	100.0	58	12	Q9E0U6	Q9E0U6 hepatitis b
37	55	100.0	58	12	Q9E0Q0	Q9E0Q0 hepatitis b
38	55	100.0	58	12	Q9E0Q6	Q9E0Q6 hepatitis b
39	55	100.0	58	12	Q9E0W4	Q9E0W4 hepatitis b
40	55	100.0	58	12	Q9E0S0	Q9E0S0 hepatitis b
41	55	100.0	58	12	Q9E0V8	Q9E0V8 hepatitis b
42	55	100.0	130	12	Q91SG7	Q91SG7 hepatitis b
43	55	100.0	130	12	Q9DKT3	Q9DKT3 hepatitis b
44	55	100.0	134	12	Q91SG6	Q91SG6 hepatitis b
45	55	100.0	134	12	Q90073	Q90073 hepatitis b

ALIGNMENTS

RESULT 1

Q9E0S8 PRELIMINARY; PRT; 58 AA.
ID Q9E0S8
AC Q9E0S8; 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
RT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
DE X protein (Fragment).
GN X
OS Hepatitis B virus.
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BSC036;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289954; AAG25247.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 58 AA; 6520 MW; 39D3CAC56C6BFE20 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;

Best Local Similarity 100.0%; Pred. No. 0.031;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLFKDWEEL 9

Db 19 CLFKDWEEL 27

RESULT 2

Q9E0Q4 PRELIMINARY; PRT; 58 AA.

ID Q9E0Q4

AC Q9E0Q4;

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DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=BBSC0324;
RT Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289966; AAG25271.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 58 AA; 6473 MW; 4ED3CAC1351248E2 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWHEEL 9
DB 19 CLFKDWHEEL 27

RESULT 3
Q9EOP6 PRELIMINARY; PRT; 58 AA.
AC Q9EOP6;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=BBSC0412;
RT Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289970; AAG25279.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 58 AA; 6464 MW; 195CADA9A4848F4 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWHEEL 9
DB 19 CLFKDWHEEL 27

RESULT 4
Q9EQU2 PRELIMINARY; PRT; 58 AA.
AC Q9EQU2;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.

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```

DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=BBSC0115;
RT Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289947; AAG25233.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 58 AA; 6487 MW; 049D70C1351248F4 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWHEEL 9
DB 19 CLFKDWHEEL 27

RESULT 5
Q9EOW2 PRELIMINARY; PRT; 58 AA.
AC Q9EOW2;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=BBSC058;
RT Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289937; AAG25213.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 58 AA; 6506 MW; 6E5CACDDFDE2FE36 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWHEEL 9
DB 19 CLFKDWHEEL 27

RESULT 6
Q9EOS4 PRELIMINARY; PRT; 58 AA.
AC Q9EOS4;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.

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OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BBSC0138;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;
 RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
 RT HBV Isolated from Patients with Hepatocellular Carcinoma and
 RT Controls";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF289956; AAG25251.1; -;
 DR InterPro: IPR000236; TransactX.
 DR Pfam: PF00739; X; 1.
 FT NON TER 1
 SQ SEQUENCE 58 AA; 6461 MW; 4ED3CADD84DF48E2 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CLFKDWEEL 9
 |||||
 DB 19 CLFKDWEEL 27

RESULT 7

Q9E0P2 PRELIMINARY; PRT; 58 AA.
 ID Q9E0P2
 AC Q9E0P2
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE x protein (Fragment).
 GN X.
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BBSC0380;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;
 RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
 RT HBV Isolated from Patients with Hepatocellular Carcinoma and
 RT Controls";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF289972; AAG25283.1; -;
 DR InterPro: IPR000236; TransactX.
 DR Pfam: PF00739; X; 1.
 FT NON TER 1
 SQ SEQUENCE 58 AA; 6490 MW; 195CACC1351248F4 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CLFKDWEEL 9
 |||||
 DB 19 CLFKDWEEL 27

RESULT 8

Q9E0S6 PRELIMINARY; PRT; 58 AA.
 ID Q9E0S6
 AC Q9E0S6
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE x protein (Fragment).
 GN X.
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=BBSC0152;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;
 RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
 RT HBV Isolated from Patients with Hepatocellular Carcinoma and
 RT Controls";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF289955; AAG25249.1; -;
 DR InterPro: IPR000236; TransactX.
 DR Pfam: PF00739; X; 1.
 FT NON TER 1
 SQ SEQUENCE 58 AA; 6487 MW; 485DACC1351248E8 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CLFKDWEEL 9
 |||||
 DB 19 CLFKDWEEL 27

RESULT 9

Q9E0U0 PRELIMINARY; PRT; 58 AA.
 ID Q9E0U0
 AC Q9E0U0
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE x protein (Fragment).
 GN X.
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BBSC0148;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;
 RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
 RT HBV Isolated from Patients with Hepatocellular Carcinoma and
 RT Controls";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF289948; AAG25235.1; -;
 DR InterPro: IPR000236; TransactX.
 DR Pfam: PF00739; X; 1.
 FT NON TER 1
 SQ SEQUENCE 58 AA; 6487 MW; 049D70C1351248F4 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CLFKDWEEL 9
 |||||
 DB 19 CLFKDWEEL 27

RESULT 10

Q9EQ02 PRELIMINARY; PRT; 58 AA.
 ID Q9EQ02
 AC Q9EQ02
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE x protein (Fragment).
 GN X.
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BBSC0354;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;

RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
 RT HBV Isolated from Patients with Hepatocellular Carcinoma and
 RT Controls.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF289967; AAG25273.1; -;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 FT NON TER 1
 SQ SEQUENCE 58 AA; 6461 MW; 4ED3CADDE4DF48E2 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLFKDWEEL 9
 Db 19 CLFKDWEEL 27

RESULT 11

Q9EON3 PRELIMINARY; PRT; 58 AA.
 AC Q9EON3
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE X protein (Fragment).
 GN X.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BBSC0396;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;
 RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
 RT HBV Isolated from Patients with Hepatocellular Carcinoma and
 RT Controls.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF289977; AAG25292.1; -;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 FT NON TER 1
 SQ SEQUENCE 58 AA; 6508 MW; ECSCACDDFE6F48EE CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLFKDWEEL 9
 Db 19 CLFKDWEEL 27

RESULT 12

Q9E0S2 PRELIMINARY; PRT; 58 AA.
 AC Q9E0S2
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE X protein (Fragment).
 GN X.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BBSHCC308;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;
 RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
 RT HBV Isolated from Patients with Hepatocellular Carcinoma and
 RT Controls.";

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF289961; AAG25261.1; -;
 DR InterPro; IPR000236; TransactX.

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF289957; AAG25253.1; -;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 FT NON TER 1
 SQ SEQUENCE 58 AA; 6494 MW; B8B3BDDDE4DF48FF CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLFKDWEEL 9
 Db 19 CLFKDWEEL 27

RESULT 13

Q9E0W6 PRELIMINARY; PRT; 58 AA.
 AC Q9E0W6
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE X protein (Fragment).
 GN X.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BBSHCC53;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;
 RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
 RT HBV Isolated from Patients with Hepatocellular Carcinoma and
 RT Controls.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF289935; AAG25209.1; -;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 FT NON TER 1
 SQ SEQUENCE 58 AA; 6464 MW; 195CACDA94A848F4 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLFKDWEEL 9
 Db 19 CLFKDWEEL 27

RESULT 14

Q9E0R4 PRELIMINARY; PRT; 58 AA.
 AC Q9E0R4
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE X protein (Fragment).
 GN X.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BBSHCC259;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;
 RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
 RT HBV Isolated from Patients with Hepatocellular Carcinoma and
 RT Controls.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF289961; AAG25261.1; -;
 DR InterPro; IPR000236; TransactX.

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DR Pfam: PF00739; X; 1.
FT NON_TER 1 1
SQ SEQUENCE 58 AA; 6478 MW; 195CACDDE4DF48F4 CRC64;

Query Match      100.0%; Score 55; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLFKDWEEL 9
Db 19 CLFKDWEEL 27

RESULT 15
Q9EOW8 PRELIMINARY; PRT; 58 AA.
AC Q9EOW8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBHCC24;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289934; AAC25208.1; --
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1 1
SQ SEQUENCE 58 AA; 6537 MW; 7ESDACDDFDE2FE36 CRC64;

Query Match      100.0%; Score 55; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLFKDWEEL 9
Db 19 CLFKDWEEL 27

Search completed: December 23, 2003, 08:46:11
Job time : 24.6 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:40:03 ; Search time 79.4 Seconds
(without alignments)
21.169 Million cell updates/sec

Title: US-09-989-621-5
Perfect score: 41
Sequence: 1 EIRLKVFL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pap.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pap.*
12: /cgn2_6/ptodata/1/pubpaa/US09C_NEW_PUB.pap.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pap.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pap.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pap.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	41	100.0	9	10	US-09-989-621-5	Sequence 5, Appli
2	37	90.2	154	15	US-10-209-264-5	Sequence 5, Appli
3	34	82.9	201	15	US-10-013-315-36	Sequence 36, Appl
4	34	82.9	476	8	US-08-834-705-4	Sequence 4, Appli
5	31	75.6	230	12	US-10-084-843-65	Sequence 65, Appl
6	31	75.6	230	12	US-10-193-002-66	Sequence 66, Appl
7	30	73.2	85	10	US-09-987-108-28	Sequence 28, Appl
8	30	73.2	589	12	US-10-205-194-144	Sequence 144, App
9	29	70.7	68	11	US-09-764-891-3030	Sequence 3030, Ap
10	29	70.7	344	9	US-09-741-669-308	Sequence 308, App
11	29	70.7	344	9	US-09-912-020-285	Sequence 285, App
12	28	68.3	57	9	US-09-864-761-37657	Sequence 37657, A
13	28	68.3	87	14	US-10-001-876-118	Sequence 118, App
14	28	68.3	98	10	US-09-861-752A-182	Sequence 182, App
15	28	68.3	156	15	US-10-074-475-237	Sequence 237, App

16	28	68.3	233	14	US-10-138-787-7	Sequence 7, Appli
17	28	68.3	238	9	US-09-904-954-2	Sequence 2, Appli
18	28	68.3	238	12	US-10-241-220-72	Sequence 72, Appl
19	28	68.3	238	12	US-09-733-756-2	Sequence 2, Appli
20	28	68.3	253	12	US-10-017-161-626	Sequence 626, App
21	28	68.3	279	9	US-09-846-808-21	Sequence 21, Appl
22	28	68.3	279	12	US-10-369-293-21	Sequence 21, Appl
23	28	68.3	279	12	US-10-285-042-21	Sequence 21, Appl
24	28	68.3	279	15	US-10-284-986-21	Sequence 21, Appl
25	28	68.3	311	10	US-09-886-055-59	Sequence 59, Appl
26	28	68.3	311	11	US-09-804-291-59	Sequence 59, Appl
27	28	68.3	311	12	US-10-387-629-82	Sequence 82, Appl
28	28	68.3	313	10	US-09-886-055-169	Sequence 169, App
29	28	68.3	313	11	US-09-804-291-169	Sequence 169, App
30	28	68.3	313	12	US-10-017-161-250	Sequence 250, App
31	28	68.3	386	12	US-10-177-478-4	Sequence 4, Appli
32	28	68.3	386	15	US-10-176-884-13	Sequence 13, Appl
33	28	68.3	401	12	US-10-094-749-2190	Sequence 2190, Ap
34	28	68.3	1152	11	US-09-374-046A-46	Sequence 46, Appl
35	27	65.9	155	14	US-10-001-835-213	Sequence 213, App
36	27	65.9	205	12	US-10-099-322-12	Sequence 12, Appl
37	27	65.9	209	9	US-09-811-284-205	Sequence 205, App
38	27	65.9	209	10	US-09-921-984-2	Sequence 2, Appli
39	27	65.9	209	14	US-10-138-787-6	Sequence 6, Appli
40	27	65.9	228	8	US-08-578-684-4	Sequence 4, Appli
41	27	65.9	228	14	US-10-138-787-9	Sequence 9, Appli
42	27	65.9	231	9	US-09-912-020-295	Sequence 295, App
43	27	65.9	307	10	US-09-886-055-381	Sequence 381, App
44	27	65.9	307	11	US-09-804-291-381	Sequence 381, App
45	27	65.9	307	12	US-10-017-161-406	Sequence 406, App

ALIGNMENTS

RESULT 1

US-09-989-621-5
; Sequence 5, Application US/09989621
; Patent No. US20020151683A1
; GENERAL INFORMATION:
; APPLICANT: Mogen Biotechnology Research Institute
; APPLICANT: Kim, Tae-Young
; APPLICANT: Lee, Ki-Young
; APPLICANT: Chang, Jin-Soo
; APPLICANT: Cho, Sung-Yoo
; APPLICANT: Hwang, Yu-Kyeong
; APPLICANT: Choi, Wyeong
; APPLICANT: Cheong, Hong-Seok
; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
; FILE REFERENCE: Derived from X Protein of Hepatitis B virus
; CURRENT APPLICATION NUMBER: US/09/989,621
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/051,006
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-989-621-5

Query Match 100.0%; Score 41; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLKVFL 9

Db 1 EIRLKVFL 9

RESULT 2

US-10-209-264-5
; Sequence 5, Application US/10209264
; Publication No. US20030003111A1
; GENERAL INFORMATION:
; APPLICANT: Oor, Chong Jin
; Lim, Gek Keow
; Zhao, Yi
; Chen, Wei Ning
; TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
; USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61 Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/209,264
; FILING DATE: 31-Jul-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/SG98/00046
; FILING DATE: 19-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J.
; REGISTRATION NUMBER: 30,086
; REFERENCE/DOCKET NUMBER: U-013109-7
; TELEPHONE: (212) 708-1800
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 154 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-209-264-5
Query Match 90.2%; Score 37; DB 15; Length 154;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IRLKVFVL 9
Db 126 IRLKIIVL 134
RESULT 3
US-10-013-315-36
; Sequence 36, Application US/10013315
; Publication No. US20030069404A1
; GENERAL INFORMATION:
; APPLICANT: Haas, Rainer
; APPLICANT: Kleanthous, Harold
; APPLICANT: Meyer, Thomas F.
; APPLICANT: Odenbreit, Stefan
; APPLICANT: Al-Garawi, Amal A.
; APPLICANT: Miller, Charles A.
; TITLE OF INVENTION: New Helicobacter Antigens and
; FILE REFERENCE: Corresponding DNA Fragments
; CURRENT APPLICATION NUMBER: US/10/013,315
; FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 08/749,051
; NUMBER OF SEQ ID NOS: 146

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-013-315-36
Query Match 82.9%; Score 34; DB 15; Length 201;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 2 IRLKVFVL 9
Db 6 VRLKIFVL 13
RESULT 4
US-08-834-705-4
; Sequence 4, Application US/08834705
; Publication No. US20030023066A1
; GENERAL INFORMATION:
; APPLICANT: Haas, Rainer et al.
; TITLE OF INVENTION: New Helicobacter Polypeptides
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,705
; FILING DATE: 01-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/749,051
; FILING DATE: 14-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,175
; REFERENCE/DOCKET NUMBER: 06132/039001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1...25
; OTHER INFORMATION:
US-08-834-705-4
Query Match 82.9%; Score 34; DB 8; Length 476;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 2 IRLKVFVL 9
Db 6 VRLKIFVL 13

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RESULT 5
US-10-084-843-65
; Sequence 65, Application US/10084843
; Publication No. US20030143243A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
;           Skeiky, Yasir A.W.
;           Dillon, Davin C.
;           Campos-Neto, Antonio
;           Houghton, Raymond
;           Vedvick, Thomas S.
;           Twardzik, Daniel R.
;           Lodes, Michael J.
;           Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
;                   AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 355
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/084,843
; FILING DATE: 25-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,967
; FILING DATE: 05-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-10-084-843-65

; Query Match 75.6%; Score 31; DB 12; Length 230;
; Best Local Similarity 44.4%; Pred. No. 79;
; Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 BIRLKVFL 9
Db 66 DVRKIFML 74

RESULT 6
US-10-193-002-66
; Sequence 66, Application US/10193002
; Publication No. US20030135026A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
;           Skeiky, Yasir A.W.
;           Dillon, Davin C.
;           Campos-Neto, Antonio
;           Houghton, Raymond

```

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;           Vedvick, Thomas S.
;           Twardzik, Daniel R.
;           Lodes, Michael J.
;           Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
;                   TUBERCULOSIS
; NUMBER OF SEQUENCES: 350
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/193,002
; FILING DATE: 10-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,596
; FILING DATE: 05-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-193-002-66

; Query Match 75.6%; Score 31; DB 12; Length 230;
; Best Local Similarity 44.4%; Pred. No. 79;
; Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 BIRLKVFL 9
Db 66 DVRKIFML 74

RESULT 7
US-09-987-108-28
; Sequence 28, Application US/09987108
; Patent No. US20020142347A1
; GENERAL INFORMATION:
; APPLICANT: KNUDSEN, Jens
; APPLICANT: WADUM, Maiken C.T.
; APPLICANT: VILLADSEN, Jens
; APPLICANT: NEERGAARD, Thomas B.F.
; TITLE OF INVENTION: BIOSENSOR
; FILE REFERENCE: KNUDSENIA
; CURRENT APPLICATION NUMBER: US/09/987,108
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/262,366
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: DK PA2000 01638
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 85
; TYPE: PRI

```

! ORGANISM: Cyprinus carpio
US-09-987-108-28

Query Match 73.2%; Score 30; DB 10; Length 85;
Best Local Similarity 55.6%; Pred. No. 45;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 22 EVLKVVFL 30

RESULT 8

US-10-205-194-144
; Sequence 144, Application US/10205194
; Publication No. US2003013430A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 5200-07-24
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: GB 0118354.0
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 144
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Rnal homolog
US-10-205-194-144

Query Match 73.2%; Score 30; DB 12; Length 589;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IRLKVFV 8
DB 180 LRLKVFV 186

RESULT 9

US-09-764-891-3030
; Sequence 3030, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3030
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-891-3030

Query Match 70.7%; Score 29; DB 11; Length 68;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 54 ELRVKDFVL 62

RESULT 10

US-09-741-669-308
; Sequence 308, Application US/09741669
; Patent No. US2002002718A1
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; TITLE OF INVENTION: Genes identified as required for
; proliferation of E. coli
; FILE REFERENCE: ELITRA.009A
; CURRENT APPLICATION NUMBER: US/09/741,669
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 60/173005
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 308
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-741-669-308

Query Match 70.7%; Score 29; DB 9; Length 344;
Best Local Similarity 55.6%; Pred. No. 3.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 2 EIRIMLFL 10

RESULT 11

US-09-912-020-285
; Sequence 285, Application US/09912020
; Patent No. US20020045592A1
; GENERAL INFORMATION:
; APPLICANT: Zyskind, Judith
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Trawick, John
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Froelich, Jamie M.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
; FILE REFERENCE: ELITRA.001DV1
; CURRENT APPLICATION NUMBER: US/09/912,020
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: 09/492,709
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/117,405
; NUMBER OF SEQ ID NOS: 485
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 285
; LENGTH: 344
; TYPE: PRT
; ORGANISM: E. Coli
US-09-912-020-285

Query Match 70.7%; Score 29; DB 9; Length 344;
Best Local Similarity 55.6%; Pred. No. 3.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 2 EIRIMLFL 10

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RESULT 12
; US-09-864-761-37657
; Sequence 37657, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aescica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37657
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010491.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.1
; OTHER INFORMATION: EST HUMAN HIT: AA133798.1, EVALUE 1.00e-22
; OTHER INFORMATION: SWISSPROT HIT: O00321, EVALUE 5.80e+00
; US-09-864-761-37657
Query Match 68.3%; Score 28; DB 9; Length 57;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

RESULT 13
; US-10-001-876-118
; Sequence 118, Application US/10001876
; Publication No. US20020177140A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Hervé
; APPLICANT: Cafferkey, Robert
; APPLICANT: Ali, Shujath
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
; FILE REFERENCE: DEX-0285
; CURRENT APPLICATION NUMBER: US/10/001,876
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,186
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 118
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-001-876-118
Query Match 68.3%; Score 28; DB 14; Length 87;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
; US-09-881-752A-182
; Sequence 182, Application US/09881752A
; Patent No. US20020115078A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Comen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; FILE REFERENCE: Encoding No. US20020115078A1el Helicobacter Polypeptides in the
; TITLE OF INVENTION: Genomone
; FILE REFERENCE: 06132/041002
; CURRENT APPLICATION NUMBER: US/09/881,752A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/833,457
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; US-09-881-752A-182
Query Match 68.3%; Score 28; DB 10; Length 98;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 EIRLKVFL 9
|:|:|:|
Db 64 EIKIEAFVL 72

RESULT 15

US-10-074-475-237
; Sequence 237, Application US/10074475
; Publication No. US20030092898A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Hu, Ping
; APPLICANT: Recipon, Herve
; APPLICANT: Kaza, Kalpana
; APPLICANT: Caferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
; FILE REFERENCE: DEX-0313
; CURRENT APPLICATION NUMBER: US/10/074,475
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 60/268,292
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 237
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-074-475-237

Query Match 68.3%; Score 28; DB 15; Length 156;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IRLKVFV 8
|:|:|:|
Db 34 VRMKVFI 40

Search completed: December 23, 2003, 08:52:50
Job time : 79.4 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 11 Seconds
(without alignments)
78.683 Million cell updates/sec

Title: US-09-989-621-5

Perfect score: 41

Sequence: 1 EIRLKVFL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	31	2 S3187	gene X protein - h
2	41	100.0	31	2 S3190	gene X protein - h
3	41	100.0	31	2 S3199	gene X protein - h
4	41	100.0	31	2 S3254	gene X protein - h
5	41	100.0	31	2 S3282	gene X protein - h
6	41	100.0	154	1 QVLD1	gene X protein - h
7	41	100.0	154	1 QVLSH	gene X protein - h
8	41	100.0	154	1 A48345	gene X protein - h
9	41	100.0	154	1 QVLAH	gene X protein - h
10	41	100.0	154	1 QVLRK	gene X protein - h
11	41	100.0	154	1 QVLRK	gene X protein - h
12	41	100.0	154	1 QVLRK	gene X protein - h
13	41	100.0	154	2 J0256	gene X protein - h
14	41	100.0	154	2 J02228	trans-activating p
15	41	100.0	154	2 S25650	gene X protein - h
16	41	100.0	154	2 J0604	gene X protein - h
17	41	100.0	154	2 S35529	gene X protein - h
18	41	100.0	154	2 S3687	gene X protein - h
19	41	100.0	154	2 S12542	gene X protein - h
20	41	100.0	154	2 S3203	gene X protein - h
21	41	100.0	154	2 S20751	gene X protein - h
22	40	97.6	31	2 S5132	gene X protein - h
23	40	97.6	31	2 S5138	gene X protein - h
24	40	97.6	31	2 S53233	gene X protein - h
25	40	97.6	31	2 S53287	gene X protein - h
26	40	97.6	154	2 S47404	gene X protein - h
27	40	97.6	154	2 J0603	gene X protein - h
28	39	95.1	31	2 S53156	gene X protein - h
29	38	92.7	31	2 S53162	gene X protein - h

ALIGNMENTS

RESULT 1

S53187
gene X protein - hepatitis B virus (isolate patient Serra'89) (fragment)
C:Species: hepatitis B virus, HBV
A:Variety: isolate patient Serra'89
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C:Accession: S53187
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A:Reference number: S53112
A:Accession: S53187
A:Molecule type: DNA
A:Residues: 1-31 <LAI>
A:Cross-references: EMBL:X85282; NID:g736084; PIDN:CAA59589.1; PID:g736085
A:Experimental source: isolate patient Serra'89
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 41; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

DB 3 EIRLKVFL 11

RESULT 2

S53190
gene X protein - hepatitis B virus (isolate patient Ferracuti'83) (fragment)
C:Species: hepatitis B virus, HBV
A:Variety: isolate patient Ferracuti'83
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C:Accession: S53190
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A:Reference number: S53112
A:Accession: S53190
A:Molecule type: DNA
A:Residues: 1-31 <LAI>
A:Cross-references: EMBL:X85283; NID:g736088; PIDN:CAA59592.1; PID:g736089
A:Experimental source: isolate patient Ferracuti'83
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 41; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

A;Experimental source: isolate patient Bio'90

C;Genetics:

A;Gene: X

C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 41; DB 1; Length 154;

Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

Db 126 EIRLKVFL 134

RESULT 8

Gene X protein - hepatitis B virus

C;Species: hepatitis B virus, HBV

C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999

C;Accession: A48345

R;Repp, R.; Keller, C.; Borkhardt, A.; Csecke, A.; Schaefer, S.; Gerlich, W.H.; Lampert,

Arch. Virol. 125, 299-304, 1992

A;Title: Detection of a hepatitis B virus variant with a truncated X gene and enhancer

A;Reference number: A48345; MUID:92352333; PMID:1642555

A;Accession: A48345

A;Molecule type: DNA

A;Residues: 1-154 <REP>

A;Cross-references: GB:S41175; NID:9252539; PIDN:AAB22732.1; PID:9252540

A;Note: sequence extracted from NCBI backbone (NCBI:109912, NCBI:109913)

C;Genetics:

A;Gene: X

C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 41; DB 1; Length 154;

Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

Db 126 EIRLKVFL 134

RESULT 9

Gene X protein - hepatitis B virus (subtype adw and adw2)

C;Species: hepatitis B virus, HBV

C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 30-Jun-1998

C;Accession: A31289; B9409; A03719

R;Lo, S.J.; Chien, W.L.; Lee, Y.H.W.

Virology 167, 289-292, 1989

A;Title: Characteristics of the X gene of hepatitis B virus.

A;Reference number: A31289; MUID:89045656; PMID:3188399

A;Accession: A31289

A;Molecule type: DNA

A;Residues: 1-154 <LOS>

A;Experimental source: subtype adw

R;Valenzuela, P.; Quiroga, M.; Zaldivar, J.; Gray, P.; Rutter, W.J.

in Animal Virus Genetics, Field, B.N., Jaenisch, R., and Fox, C.F., eds., pp.57-70, Acad

A;Reference number: A94409

A;Accession: B94409

A;Molecule type: DNA

A;Residues: 1-154 <VAL>

A;Experimental source: subtype adw2

C;Genetics:

A;Gene: X

C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 41; DB 1; Length 154;

Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

Db 126 EIRLKVFL 134

Db 126 EIRLKVFL 134

RESULT 10

Gene X protein - hepatitis B virus (subtype adw, strain 991)

C;Species: hepatitis B virus, HBV

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999

C;Accession: S10380

R;Koechel, H.G.; Schueler, A.; Lottmann, S.; Thomssen, R.

submitted to the EMBL Data Library, February 1990

A;Reference number: S10380

A;Accession: S10380

A;Molecule type: DNA

A;Residues: 1-154 <KOE>

A;Cross-references: EMBL:X51970; NID:gi155012; PIDN:CAA36231.1; PID:g60432

C;Genetics:

A;Gene: X

C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 41; DB 1; Length 154;

Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

Db 126 EIRLKVFL 134

RESULT 11

Gene X protein - hepatitis B virus (strain LSH, chimpanzee)

C;Species: hepatitis B virus, HBV

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jun-2000

C;Accession: D28885

R;Vaudin, M.; Wolstenholme, A.J.; Tsiquaye, K.N.; Zuckerman, A.J.; Harrison, T.J.

J. Gen. Virol. 69, 1383-1389, 1988

A;Title: The complete nucleotide sequence of the genome of a hepatitis B virus isolated

A;Reference number: A92796; MUID:88258473; PMID:2838576

A;Accession: D28885

A;Molecule type: DNA

A;Residues: 1-154 <VAU>

A;Cross-references: GB:D00220; NID:g221505; PIDN:BAA00160.1; PID:g221509

C;Genetics:

A;Gene: X

C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 41; DB 1; Length 154;

Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

Db 126 EIRLKVFL 134

RESULT 12

Gene X protein - hepatitis B virus (subtype ayw, patient B)

C;Species: hepatitis B virus, HBV

A;Variety: subtype ayw, patient B

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C;Accession: S20756

R;Jai, M.E.; Mazoleni, A.P.; Balestrieri, A.; Mellis, A.; Porru, A.

submitted to the EMBL Data Library, March 1992

A;Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negati

A;Reference number: S20745

A;Accession: S20756

A;Molecule type: DNA

A;Residues: 1-154 <LAI>

A;Cross-references: EMBL:X65259; NID:g59439; PIDN:CAA46360.1; PID:g59443

A;Experimental source: subtype ayw, patient E

C;Genetics:

```

A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 41; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 126 EIRLKVFL 134

RESULT 13
JS0256
gene X protein - hepatitis B virus (subtype adv, strain Japan/pJ2W233)
C:Species: hepatitis B virus, HBV
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 14-Nov-1997
C:Accession: JS0256
R:Okamoto, H.; Tsuda, F.; Sakugawa, H.; Sastrocewignjo, R.I.; Imai, M.; Miyakawa, Y.; M
J. Gen. Virol. 69, 2575-2583, 1988
A:Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of sur
A:Reference number: JS0253; MUID:89010694; PMID:3171552
A:Accession: JS0256
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-154 <OKA>
A:Cross-references: GB:D00329; NID:G221497
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 41; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 126 EIRLKVFL 134

RESULT 14
JQ2228
trans-activating protein X - hepatitis B virus
N:Alternate names: HBx protein
C:Species: hepatitis B virus, HBV
C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 26-Aug-1999
C:Accession: JQ2228; S31794
R:Naumann, H.; Schaefer, S.; Yoshida, C.F.T.; Gaspar, A.M.C.; Repp, R.; Gerlich, W.H.
J. Gen. Virol. 74, 1627-1632, 1993
A:Title: Identification of a new hepatitis B virus (HBV) genotype from Brazil that expre
A:Reference number: JQ2225; MUID:93346970; PMID:8345355
A:Accession: JQ2228
A:Molecule type: DNA
A:Residues: 1-154 <NAU>
A:Cross-references: EMBL:X69798; NID:G59422; PIDN:CAA49453.1; PID:G59424
C:Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 41; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 126 EIRLKVFL 134

RESULT 15
S25650
gene X protein - hepatitis B virus (subtype ayw, patient D)
C:Species: hepatitis B virus, HBV
A:Variety: subtype ayw, patient D
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S25650

```

R:Lai, M.E.; Mazzoleni, A.P.; Melis, A.; Balestrieri, A.
submitted to the EMBL Data Library, September 1992
A:Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negat
A:Reference number: S25650
A:Accession: S25650
A:Molecule type: DNA
A:Residues: 1-154 <LAI>
A:Cross-references: EMBL:X68292; NID:G59448; PIDN:CAA48352.1; PID:G59449
A:Experimental source: subtype ayw, patient D
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 41; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 126 EIRLKVFL 134

Search completed: December 23, 2003, 08:41:09
Job time : 11 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 6.4 seconds
(without alignments)
66.131 Million cell updates/sec

Title: US-09-989-621-5
Perfect score: 41
Sequence: 1 EIRLKVFL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	154	1 X_HPBV2	P03166 hepatitis b
2	41	100.0	154	1 X_HPBV4	P12936 hepatitis b
3	41	100.0	154	1 X_HPBV9	P17102 hepatitis b
4	41	100.0	154	1 X_HPBVT	P20975 hepatitis b
5	41	100.0	154	1 X_HPBVJ	P20976 hepatitis b
6	41	100.0	154	1 X_HPBVL	P12912 hepatitis b
7	41	100.0	154	1 X_HPBVT	P05499 hepatitis b
8	41	100.0	154	1 X_HPBVT	P03165 hepatitis b
9	40	97.6	154	1 X_HPBVO	P20977 hepatitis b
10	34	82.9	154	1 X_HPBVA	P24026 hepatitis b
11	33	80.5	179	1 NUGC_SINY3	P19125 synchocyst
12	31	75.6	175	1 NUGC_ANASP	Q44241 anabaena sp
13	31	75.6	175	1 NUGC_ANAVA	Q9xb16 anabaena va
14	31	75.6	267	1 Y123_THEMA	Q9wx77 thetmotoga
15	30	73.2	100	1 VE7_HPV38	Q80908 human papil
16	30	73.2	102	1 VE7_HPV36	P50811 human papil
17	30	73.2	223	1 RPE_ECOLI	P12972 escherichia
18	30	73.2	230	1 RPE_VIBCH	Q8kt51 vibrio chol
19	30	73.2	589	1 RGP1_MOUSE	P46061 mus musculus
20	29	70.7	102	1 VE7_HPV25	P36823 human papil
21	29	70.7	103	1 VE7_HPV05	P06932 human papil
22	29	70.7	103	1 VE7_HPV47	P22423 human papil
23	29	70.7	103	1 VE7_HPV49	P36830 human papil
24	29	70.7	103	1 VE7_HPV5B	P26559 human papil
25	29	70.7	138	1 X_HPBGS	P03148 ground squi
26	29	70.7	169	1 NUGC_MARPO	P33340 marchantia
27	29	70.7	344	1 YHXA_ECOLI	P33340 escherichia
28	29	70.7	373	1 ADHA_RABIT	O19053 coryctolagus
29	29	70.7	430	1 MTS9_STAAU	P23737 staphylococ
30	29	70.7	564	1 ATKA_PSEAE	P57683 pseudomonas
31	29	70.7	926	1 CTF4_YEAST	Q01454 saccharomyc
32	28	68.3	187	1 RPA3_MOUSE	O08545 mus musculus
33	28	68.3	199	1 YD66_YEAST	P38962 saccharomyc

RESULT 1

ID	X_HPBV2	STANDARD;	PRT;	154 AA.
AC	P03166; P12935;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, last sequence update)			
DT	15-DEC-1998 (Rel. 37, last annotation update)			
DE	Trans-activating protein X.			
GN	X.			
OS	Hepatitis B virus (subtype adw2), and			
OS	Hepatitis B virus (subtype adw).			
OC	Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.			
OX	NCBI_TaxID=10408, 106821;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ADW2;			
RA	Valenzuela P., Quiroga M., Zaldivar J., Gray P., Rutter W.J.;			
RL	(In) Field B.N., Jaenisch R., Fox C.F. (eds.);			
RL	Animal Virus Genetics, pp.57-70, Academic Press, New York (1980).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ADW;			
RX	MEDLINE=89045656; PubMed=3188399;			
RA	Lo S.J., Chien M.L., Lee Y.H.W.;			
RL	"Characteristics of the X gene of hepatitis B virus.;"			
RL	Virology 167:289-292(1988).			
RP	[3]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN=ADW;			
RA	MEDLINE=83168919; PubMed=6300776;			
RA	Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;			
RT	"The complete nucleotide sequences of the cloned hepatitis B virus			
RT	DNA; subtype adr and adw.;"			
RL	Nucleic Acids Res. 11:1747-1757(1983).			
CC	-!- FUNCTION: INDISENSIBLE FOR HBV REPLICATION IN VIVO.			
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CC	-----			
DR	EMBL; X02763; CAA26540.1; -			
DR	EMBL; Z35717; CAA84789.1; -			
DR	EMBL; M23692; AAA56820.1; -			
DR	EMBL; V00866; -; NOT_ANNOTATED_CDS.			
DR	PIR; A31289; QOVLAW.			
DR	PIR; S47408; S47408.			
DR	InterPro; IPR000236; TransactX.			
DR	Pfam; PF00739; X; 1.			
FT	CONFLICT 80 80 E -> A (IN REF. 3).			
FT	CONFLICT 115 115 C -> S (IN REF. 2).			
FT	CONFLICT 130 131 KV -> MI (IN REF. 3).			
FT	CONFLICT 154 AA; 16583 MW; 7F2AE32A4F025670 CRC64;			
SQ	SEQUENCE			

P52797 homo sapien
P97055 rhodobacter
P74921 thermotoga
Q9c8a4 mycobacteri
Q8r6c8 fusobacteri
Q8wz94 homo sapien
P52048 escherichia
Q9jkc7 mus musculus
O00189 homo sapien
P33374 alcaligenes
P38250 saccharomyc
Q15393 homo sapien

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Query Match      100.0%; Score 41; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 126 EIRLKVFL 134

RESULT 2
X HPBV4
ID X HPBV4 STANDARD; PRT; 154 AA.
AC PI2936;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adr4).
OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10409;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83246570; PubMed=6306594;
RA Fujiyama A., Miyahara A., Nozaki C., Yoneyama T., Ontomo N.,
RA Matsubara K.;
RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype
RT adr";
RL Nucleic Acids Res. 11:4601-4610(1983).
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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CC
CC EMBL; X01587; CAA25744.1;
CC InterPro; IPR000236; TransactX.
CC Pfam; PF00739; X; 1.
CC SEQUENCE 154 AA; 16622 MW; 594A1D0718928804 CRC64;

Query Match      100.0%; Score 41; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 126 EIRLKVFL 134

RESULT 3
X HPBV9
ID X HPBV9 STANDARD; PRT; 154 AA.
AC PI7102;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adr / strain 991).
OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10410;
RN [1]
RP SEQUENCE FROM N.A.
RX Koechel H.G., Schueler A., Lottmann S., Thomssen R.;
RX Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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CC
CC EMBL; X51970; CAA36231.1;
CC InterPro; IPR000236; TransactX.
CC Pfam; PF00739; X; 1.
CC SEQUENCE 154 AA; 16553 MW; 52A0D9CEFE6DCDE0 CRC64;

Query Match      100.0%; Score 41; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 126 EIRLKVFL 134

RESULT 4
X HPBEV1
ID X HPBEV1 STANDARD; PRT; 154 AA.
AC P20975;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw / strain Indonesia/p1DW420).
OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10412;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RX Okamoto H., Tsuda F., Sakugawa H., Sastroroenigjo R.I., Imai M.,
RX Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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CC
CC EMBL; D00331; NOT_ANNOTATED_CDS.
CC InterPro; IPR000236; TransactX.
CC Pfam; PF00739; X; 1.
CC SEQUENCE 154 AA; 16556 MW; C80C817E961BFFB9 CRC64;

Query Match      100.0%; Score 41; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 126 EIRLKVFL 134

RESULT 5
X HPBVJ
ID X HPBVJ STANDARD; PRT; 154 AA.
AC P20976;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

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DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw / strain Japan/PJRW233).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10413;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Teuda F., Sakugawa H., Sastroseowignjo R.I., Imai M.,
RA Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
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CC -----
DR EMBL; D00329; ; NOT_ANNOTATED_CDS.
DR PIR; J50256; JS0256;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
DR SEQUENCE 154 AA; 16595 MW; 512ASAO77169D5CA CRC64;
SQ
Query Match 100.0%; Score 41; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKVFL 9
DB 126 EIRLKVFL 134
RESULT 6
X_HPBVL STANDARD; PRT; 154 AA.
AC
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (strain lsh / chimpanzee isolate).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10414;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88258473; PubMed=2838576;
RA Vaudin M., Wolstenholme A.J., Tsiquaye K.N., Zuckerman A.J.,
RA Harrison T.J.;
RT "The complete nucleotide sequence of the genome of a hepatitis B
RT virus isolated from a naturally infected chimpanzee.";
RL J. Gen. Virol. 69:1383-1389(1988).
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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CC -----
DR EMBL; D00220; BAA00160.1; -
DR PIR; D28885; QOVLCP.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ
SEQUENCE 154 AA; 16759 MW; F6C9D7D30C16D743 CRC64;
Query Match 100.0%; Score 41; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKVFL 9
DB 126 EIRLKVFL 134
RESULT 7
X_HPBVL STANDARD; PRT; 154 AA.
AC
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw4 / strain Brazil / isolate w4B).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=45410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93346970; PubMed=8345355;
RA Naumann H., Schaefer S., Yoshida C.F.T., Gaspar A.M.C., Repp R.,
RA Gerlich W.H.;
RT "Identification of a new hepatitis B virus (HBV) genotype from Brazil
RT that expresses HBV surface antigen subtype adw4.";
RL J. Gen. Virol. 74:1627-1632(1993).
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DR EMBL; X59798; CAA49453.1; -
DR PIR; JQ2228; JQ2228.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
DR SEQUENCE 154 AA; 16715 MW; E523C051B9B0B737 CRC64;
SQ
Query Match 100.0%; Score 41; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKVFL 9
DB 126 EIRLKVFL 134
RESULT 8
X_HPBVL STANDARD; PRT; 154 AA.
AC
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype ayw).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10418;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012091; PubMed=399327;
RA Galibert F., Mandart E., Pitoussi F., Tiollais P., Charnay P.;
RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)

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RT cloned in E. coli";
RL Nature 281:646-650(1979).
RN [2].
RP SEQUENCE FROM N.A.
RC STRAIN=Latvia;
RX MEDLINE=85204397; PubMed=3996597;
RA Bichko V., Dreilina D., Pushko P.M., Pumpen P.P., Gren E.;
RT "Subtype ayw variant of hepatitis B virus. DNA primary structure
analysis";
RL FEBS Lett. 185:208-212(1985).
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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CC
CC EMBL; V01460; -; NOT ANNOTATED_CDS.
DR EMBL; X02496; CAB41657.1; -;
DR PIR; A03719; QOVLDI.
DR PIR; A05237; QOVLH.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
DR VARIANT 46 46 P -> S (IN STRAIN LATVIA).
FT VARIANT 84 88 NAHQI -> KAOPF (IN STRAIN LATVIA).
FT VARIANT 102 102 A -> V (IN STRAIN LATVIA).
FT CONFLICT 26 26 R -> C (IN REF. 1).
SQ SEQUENCE 154 AA; 16618 MW; 29FD1CC9E09A34B5 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 126 EIRLKVFL 134

RESULT 9
X HPBVO STANDARD; PRT; 154 AA.
AC P20977;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw / strain Okinawa/P0DW282).
OC Viruses; Retroviridae; Orthohepadnavirus.
OX NCBI_TaxID=10415;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosaswignjo R.I., Imai M.,
RA Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
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CC
CC EMBL; D00330; -; NOT ANNOTATED_CDS.
DR EMBL; J50603; J50603.
DR PIR; J50603; J50603.

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DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16558 MW; E2646C059A30125F CRC64;

Query Match 97.6%; Score 40; DB 1; Length 154;
Best Local Similarity 88.9%; Pred. No. 0.05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 126 EIRLKVFL 134

RESULT 10
X HPBVA STANDARD; PRT; 154 AA.
ID X HPBVA STANDARD; PRT; 154 AA.
AC P24026;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (strain alpha1).
OC Viruses; Retroviridae; Orthohepadnavirus.
OX NCBI_TaxID=10411;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90266476; PubMed=2345966;
RA Tong S., Li J., Vitvitski L., Trepo C.;
RT "Active hepatitis B virus replication in the presence of anti-HBe is
RT associated with viral variants containing an inactive pre-C region.";
RL Virology 176:596-603(1990).
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
CC
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CC
CC EMBL; M32138; AAA45504.1; -;
DR EMBL; D34773; QOVLAI.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16671 MW; 2CFEEA77FA5E271F CRC64;

Query Match 82.9%; Score 34; DB 1; Length 154;
Best Local Similarity 77.8%; Pred. No. 1.3;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 126 EIRLKVFL 134

RESULT 11
NUGC SYN3 STANDARD; PRT; 179 AA.
ID NUGC SYN3 STANDARD; PRT; 179 AA.
AC P19125; P74194;
DT 01-NOV-1990 (Rel. 16, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NAD(P)H-guanylate oxidoreductase subunit J (EC 1.6.5.-) (NAD(P)H
DE dehydrogenase I, subunit J) (NDH-1, subunit J) (ORF 155).
GN NDHJ OR SLR1281.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89281491; PubMed=2499764;

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RA Steinmueller K., Ley A.C., Steinmetz A.A., Sayre R.T., Bogorad L.;
RT "Characterization of the ndhC-psbG-ORF157/159 operon of maize plastid
RL DNA and of the cyanobacterium Synechocystis sp. PCC6803.";
RN Mol. Gen. Genet. 216:60-69(1998).
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpō S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- FUNCTION: NDH-1 shuttles electrons from NAD(P)H, via FMN and iron-
CC sulfur (Fe-S) centers, to quinones in the respiratory chain. The
CC immediate electron acceptor for the enzyme in this species is
CC believed to be plastoquinone. Couples the redox reaction to proton
CC translocation (for every two electrons transferred, four hydrogen
CC ions are translocated across the cytoplasmic membrane), and thus
CC conserves the redox energy in a proton gradient.
CC -1- CATALYTIC ACTIVITY: NAD(P)H + plastoquinone = NAD(P)(+) +
CC plastoquinol.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I 30 kDa SUBUNIT FAMILY.
CC -----
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CC -----
CC EMBL: X17439; CAA35486.1; ALT_INIT.
CC DDBJ: D90913; BAA18285.1;
CC PIR: S7826; S7826.
CC InterPro: IPR001268; Complex1_30K.
CC Pfam: PF00329; complex1_30Kd; 1.
CC ProDom: PD001581; Complex1_30K; 1.
CC PROSITE: PS00542; COMPLEX1_30K; 1.
CC Oxidoreductase; NAD; NADP; Quinone; Plastoquinone; Complete proteome.
CC SEQUENCE 179 AA; 20593 MW; 3EE18D5E727F8BCC CRC64;
Query Match 80.5%; Score 33; DB 1; Length 179;
Best Local Similarity 75.0%; Pred. No. 2.5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Y 1 EIRLKVFV 8
b 104 EVRLKVFV 111
RESULT 12
JUGC ANASP
ID NUGC ANASP STANDARD; PRT; 175 AA.
AC Q44241; Q9WN0;
AT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NAD(P)H-quinone oxidoreductase subunit J (EC 1.6.5.-) (NAD(P)H
DE dehydrogenase I, subunit J) (NDH-1, subunit J) (NDH-J).
EN NDHJ OR AL13840.
XS Anabaena sp. (strain PCC 7120).
XN Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
XX NCBI_TaxId=103690;
XP [1]
RP SEQUENCE FROM N.A.
RA Happe T., Schiefer W., Boehme H.;
RT "Isolation and characterisation of the ndhCKJ-cluster of the
RT cyanobacteria Anabaena sp. PCC 7120.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

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RN SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpō S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
RN [3]
RP SEQUENCE OF 1-155 FROM N.A.
RX MEDLINE=96390878; PubMed=8797851;
RA Howitt C.A., Whelan J., Price G.D., Day D.A.;
RT "Cloning, analysis and inactivation of the ndhK gene encoding a
RT subunit of NADH quinone oxidoreductase from Anabaena PCC 7120.";
CC Eur. J. Biochem. 240:173-180(1996).
CC -1- FUNCTION: NDH-1 shuttles electrons from NAD(P)H, via FMN and iron-
CC sulfur (Fe-S) centers, to quinones in the respiratory chain. The
CC immediate electron acceptor for the enzyme in this species is
CC believed to be plastoquinone. Couples the redox reaction to proton
CC translocation (for every two electrons transferred, four hydrogen
CC ions are translocated across the cytoplasmic membrane), and thus
CC conserves the redox energy in a proton gradient (By similarity).
CC -1- CATALYTIC ACTIVITY: NAD(P)H + plastoquinone = NAD(P)(+) +
CC plastoquinol.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I 30 kDa SUBUNIT FAMILY.
CC -----
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CC -----
CC EMBL: AJ012180; CAB45641.1;
CC DDBJ: AP003594; BAB75539.1;
CC PIR: U32208; AAC44354.1; ALT_INIT.
CC InterPro: IPR001268; Complex1_30K.
CC Pfam: PF00329; complex1_30Kd; 1.
CC ProDom: PD001581; Complex1_30K; 1.
CC PROSITE: PS00542; COMPLEX1_30K; 1.
CC Oxidoreductase; NAD; NADP; Quinone; Plastoquinone; Complete proteome.
CC CONFLICT 7 14 EA -> K (IN REF. 3).
CC CONFLICT 13 50 A -> P (IN REF. 3).
CC CONFLICT 53 53 L -> M (IN REF. 3).
CC CONFLICT 74 74 V -> I (IN REF. 3).
CC CONFLICT 101 101 I -> V (IN REF. 3).
CC CONFLICT 152 152 E -> G (IN REF. 3).
CC SEQUENCE 175 AA; 19893 MW; FA257DBD976D3A4 CRC64;
Query Match 75.6%; Score 31; DB 1; Length 175;
Best Local Similarity 75.0%; Pred. No. 7.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Y 1 EIRLKVFV 8
b 100 EIRKVFV 107
RESULT 13
NUGC ANAVA
ID NUGC ANAVA STANDARD; PRT; 175 AA.
AC Q9XBL6;
AT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NAD(P)H-quinone oxidoreductase subunit J (EC 1.6.5.-) (NAD(P)H
DE dehydrogenase I, subunit J) (NDH-1, subunit J).

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GN NDHJ.
OS Anabaena variabilis.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=1172;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=POC 7937 / ATCC 29413;
RA Happe T., Schiefer W., Boehme H.;
RT "Isolation and characterisation of the ndhCKJ gene-cluster of Anabaena
RL variabilis".
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: NDH-1 shuttles electrons from NAD(P)H, via FMN and iron-
CC sulfur (Fe-S) centers, to quinones in the respiratory chain. The
CC immediate electron acceptor for the enzyme in this species is
CC believed to be plastoquinone. Couples the redox reaction to proton
CC translocation (for every two electrons transferred, four hydrogen
CC ions are translocated across the cytoplasmic membrane), and thus
CC conserves the redox energy in a proton gradient (By similarity).
CC -1- CATALYTIC ACTIVITY: NAD(P)H + plastoquinone = NAD(P)H(+) +
CC plastoquinol.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I 30 kDa SUBUNIT FAMILY.
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CC EMBL; AJ012181; CAB45648.1; -
CC InterPro; IPR001268; Complex1_30K.
CC Pfam; PF00329; complex1_30K; 1.
CC ProDom; PD001591; Complex1_30K; 1.
CC PROSITE; PS00542; COMPLEX1_30K; FALSE_NEG.
CC Oxidoreductase; NAD; NADP; Quinone; Plastoquinone.
CC KW OXIDOREDUCTASE; NAD; NADP; Quinone; Plastoquinone.
CC FT SEQUENCE 175 AA; 19949 MW; F902147E12EA1640 CRC64;
SQ
Query Match 75.6%; Score 31; DB 1; Length 175;
Best Local Similarity 75.0%; Pred. No. 7.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKVFL 8
DB 100 EIRKVFL 107
RESULT 14
Y123 THEM
ID Y123 THEM STANDARD; PRT; 267 AA.
AC QWXX7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DB Putative periplasmic metal-binding protein TM0123 precursor.
GN TM0123.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RA MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwynn M.L., Dodson R.J.,
RA Haft D.H., Hickley E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Sutton W.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RL genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
CC -1- FUNCTION: PART OF AN ATP-DRIVEN TRANSPORT SYSTEM

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CC TM0123/TM0124/TM0125 FOR A METAL. METAL-BINDING COMPONENT.
CC -1- SUBCELLULAR LOCATION: Periplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL SOLUTE-BINDING PROTEIN FAMILY
CC 9.
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CC EMBL; AB001698; AAD35217.1; -
CC PIR; C72415; C72415.
CC HSP; P96116; ITOA.
CC TIGR; TM0123; -
CC InterPro; IPR006128; Lipoprotein_4.
CC InterPro; IPR006127; SBP_bac_9.
CC Pfam; PF01297; SBP_bac_9; 1.
CC PRINTS; PR00690; ADHESNFAMILY.
CC KW Hypothetical protein; Transport; Periplasmic; Metal-binding; Signal;
CC FT SIGNAL 1 15 POTENTIAL.
CC CHAIN 16 267 PUTATIVE PERIPLASMIC METAL-BINDING
CC PROTEIN TM0123.
CC FT SEQUENCE 267 AA; 30144 MW; 35ADDF6003C22A6 CRC64;
SQ
Query Match 75.6%; Score 31; DB 1; Length 267;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EIRLKVFL 9
DB 232 EIRKSFVL 240
RESULT 15
V07 HPV38
ID V07 HPV38 STANDARD; PRT; 100 AA.
AC Q80308;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE E7 protein.
GN E7.
OS Human papillomavirus type 38.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=37959;
RN [1]
RP SEQUENCE FROM N.A.
RA Delius H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: E7 PROTEIN HAS BOTH TRANSFORMING AND TRANS-ACTIVATING
CC ACTIVITIES
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CC EMBL; U01787; AAA79451.1; -
CC InterPro; IPR000148; Papvi_E7.
CC Pfam; PF00527; E7; 1.
CC KW Early protein; Transcription regulation; Oncogene;
CC DNA-binding; Trans-acting factor.
CC SITE 55 58 C-XX-C MOTIF-1.
CC SITE 88 91 C-XX-C MOTIF-2.
CC SEQUENCE 100 AA; 11261 MW; C56F5E14A8E978D CRC64;
SQ

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Query Match 73.2%; Score 30; DB 1; Length 100;
Best Local Similarity 62.5%; Pred. No. 6.9;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVTV 8

DB 59 EVRLKLYV 66

Search completed: December 23, 2003, 08:41:54
Job time : 8.4 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:58 ; Search time 23.6 Seconds
(without alignments)
98.410 Million cell updates/sec

Title: US-09-989-621-5
Perfect score: 41 EIRLKFVL 9
Sequence: 1 EIRLKFVL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacterioph:
17: sp_archaea:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	30	12	Q9QS36 hepatitis b
2	41	100.0	30	12	Q9QS33 hepatitis b
3	41	100.0	30	12	Q9QS45 hepatitis b
4	41	100.0	30	12	Q9QS47 hepatitis b
5	41	100.0	30	12	Q9QS40 hepatitis b
6	41	100.0	30	12	Q9QS19 hepatitis b
7	41	100.0	30	12	Q9QS29 hepatitis b
8	41	100.0	30	12	Q9QS50 hepatitis b
9	41	100.0	30	12	Q9QS37 hepatitis b
10	41	100.0	30	12	Q9QS27 hepatitis b
11	41	100.0	30	12	Q9QS30 hepatitis b
12	41	100.0	30	12	Q9QS44 hepatitis b
13	41	100.0	30	12	Q9QS42 hepatitis b
14	41	100.0	31	12	Q9QS42 hepatitis b
15	41	100.0	31	12	Q9QS42 hepatitis b
16	41	100.0	31	12	Q9QS42 hepatitis b

17	41	100.0	31	12	Q67992 hepatitis b
18	41	100.0	31	12	Q68002 hepatitis b
19	41	100.0	31	12	Q68050 hepatitis b
20	41	100.0	31	12	Q68004 hepatitis b
21	41	100.0	31	12	Q68019 hepatitis b
22	41	100.0	31	12	Q68056 hepatitis b
23	41	100.0	31	12	Q68011 hepatitis b
24	41	100.0	31	12	Q68066 hepatitis b
25	41	100.0	31	12	Q68071 hepatitis b
26	41	100.0	31	12	Q68071 hepatitis b
27	41	100.0	31	12	Q68046 hepatitis b
28	41	100.0	31	12	Q68052 hepatitis b
29	41	100.0	31	12	Q68029 hepatitis b
30	41	100.0	31	12	Q68067 hepatitis b
31	41	100.0	31	12	Q68044 hepatitis b
32	41	100.0	31	12	Q68039 hepatitis b
33	41	100.0	31	12	Q68039 hepatitis b
34	41	100.0	31	12	Q68076 hepatitis b
35	41	100.0	31	12	Q68076 hepatitis b
36	41	100.0	31	12	Q68072 hepatitis b
37	41	100.0	31	12	Q68047 hepatitis b
38	41	100.0	31	12	Q68043 hepatitis b
39	41	100.0	31	12	Q68028 hepatitis b
40	41	100.0	31	12	Q68028 hepatitis b
41	41	100.0	31	12	Q68074 hepatitis b
42	41	100.0	31	12	Q68074 hepatitis b
43	41	100.0	31	12	Q68062 hepatitis b
44	41	100.0	31	12	Q68054 hepatitis b
45	41	100.0	31	12	Q68031 hepatitis b

ALIGNMENTS

RESULT 1

Q9QS36 PRELIMINARY; PRT; 30 AA.
ID Q9QS36
AC Q9QS36;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillon A.P., Norstrom G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers.";
RL J. Infect. Dis. 179:775-782(1999).
DR EMBL; AF106106; AAD46440.1;
DR InterPro; IPR00236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1 30
SQ SEQUENCE 30 AA; 3421 MW; 6B4CAB70901228E CRC64;

Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKFVL 9
Db 10 EIRLKFVL 18

RESULT 2

Q9QS53 PRELIMINARY; PRT; 30 AA.
ID Q9QS53
AC Q9QS53;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillion A.P., Norkrans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers.";
RL J. Infect. Dis. 179:775-782(1999).
DR EMBL; AF106089; AAD46423.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1 1
FT NON TER 30 30
SQ SEQUENCE 30 AA; 3457 MW; 3AA3AE6709012298 CRC64;
Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKVFL 9
DB 10 EIRLKVFL 18
RESULT 3
Q9QS45
ID Q9QS45 PRELIMINARY; PRT; 30 AA.
AC Q9QS45
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillion A.P., Norkrans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers.";
RL J. Infect. Dis. 179:775-782(1999).
DR EMBL; AF106097; AAD46431.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1 1
FT NON TER 30 30
SQ SEQUENCE 30 AA; 3447 MW; 3AA3ACE709012298 CRC64;
Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKVFL 9
DB 10 EIRLKVFL 18
RESULT 4
Q9QS47
ID Q9QS47 PRELIMINARY; PRT; 30 AA.
AC Q9QS47
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillion A.P., Norkrans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers.";
RL J. Infect. Dis. 179:775-782(1999).
DR EMBL; AF106095; AAD46429.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1 1
FT NON TER 30 30
SQ SEQUENCE 30 AA; 3447 MW; 3AA3ACE709012298 CRC64;
Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKVFL 9
DB 10 EIRLKVFL 18
RESULT 5
Q9QS40
ID Q9QS40 PRELIMINARY; PRT; 30 AA.
AC Q9QS40
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillion A.P., Norkrans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers.";
RL J. Infect. Dis. 179:775-782(1999).
DR EMBL; AF106102; AAD46436.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1 1
FT NON TER 30 30
SQ SEQUENCE 30 AA; 3447 MW; 3AA3ACE709012298 CRC64;
Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKVFL 9
DB 10 EIRLKVFL 18
RESULT 6
Q9QS19
ID Q9QS19 PRELIMINARY; PRT; 30 AA.
AC Q9QS19
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
EX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillon A.P., Norrkans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers";
RL J. Infect. Dis. 179:775-782(1999).
DR EMBL; AF106123; AAD46457.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
FT NON_TER 30
SQ SEQUENCE 30 AA; 3460 MW; 3AA3ACB607E1CD98 CRC64;
Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKVFL 9
DB 10 EIRLKVFL 18
RESULT 7
Q9QS29 PRELIMINARY; PRT; 30 AA.
ID Q9QS29
AC Q9QS29
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
EX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillon A.P., Norrkans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers";
RL J. Infect. Dis. 179:775-782(1999).
DR EMBL; AF106113; AAD46447.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
FT NON_TER 30
SQ SEQUENCE 30 AA; 3460 MW; 3AA3ACB607E1CD98 CRC64;
Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKVFL 9
DB 10 EIRLKVFL 18
RESULT 8
Q9QS50 PRELIMINARY; PRT; 30 AA.
ID Q9QS50
AC Q9QS50
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillon A.P., Norrkans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers";
RL J. Infect. Dis. 179:775-782(1999).
DR EMBL; AF106092; AAD46426.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
FT NON_TER 30
SQ SEQUENCE 30 AA; 3447 MW; 3AA3ACB709012298 CRC64;
Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKVFL 9
DB 10 EIRLKVFL 18
RESULT 9
Q9QS37 PRELIMINARY; PRT; 30 AA.
ID Q9QS37
AC Q9QS37
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
EX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillon A.P., Norrkans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers";
RL J. Infect. Dis. 179:775-782(1999).
DR EMBL; AF106105; AAD46439.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
FT NON_TER 30
SQ SEQUENCE 30 AA; 3447 MW; 3AA3ACB709012298 CRC64;
Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKVFL 9
DB 10 EIRLKVFL 18
RESULT 10
Q9QS27 PRELIMINARY; PRT; 30 AA.
ID Q9QS27
AC Q9QS27
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
EX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillon A.P., Norrkans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral

RT replication and liver damage in East Asian hepatitis B virus
RT carriers."
RL J. Infect. Dis. 179:775-782(1999).
DR ENBL; AF106115; AAD46449.1; --
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1 1
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3460 MW; 3AA3ACB607E1CD98 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 10 EIRLKVFL 18

RESULT 11

Q9QS30 PRELIMINARY; PRT; 30 AA.
AC Q9QS30
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillion A.P., Norrkans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers."
RL J. Infect. Dis. 179:775-782(1999).
DR ENBL; AF106112; AAD46446.1; --
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1 1
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3460 MW; 3AA3ACB607E1CD98 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 10 EIRLKVFL 18

RESULT 12

Q9QS44 PRELIMINARY; PRT; 30 AA.
AC Q9QS44
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillion A.P., Norrkans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers."
RL J. Infect. Dis. 179:775-782(1999).

DR ENBL; AF106098; AAD46432.1; --
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1 1
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3447 MW; 3AA3ACB709012298 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 10 EIRLKVFL 18

RESULT 13

Q9QS42 PRELIMINARY; PRT; 30 AA.
AC Q9QS42
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillion A.P., Norrkans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers."
RL J. Infect. Dis. 179:775-782(1999).
DR ENBL; AF106100; AAD46434.1; --
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1 1
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3447 MW; 3AA3ACB709012298 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 10 EIRLKVFL 18

RESULT 14

Q67967 PRELIMINARY; PRT; 31 AA.
AC Q67967
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE X, PreC and C genes (Pintus) (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
RL Submitted (MAR-1995) to the ENBL/GenBank/DBJ databases.
DR ENBL; X85287; CAA59548.1; --
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1 1
FT NON_TER 31 AA; 3364 MW; A776AB25508DEA72 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 31;
 Best Local Similarity 100.0%; Pred.No. 0.062; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
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 Db 3 EIRLKVFL 11

RESULT 15

28JSB0 PRELIMINARY; PRT; 31 AA.
 ID Q8JSB0
 AC Q8JSB0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 ST 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 PE X protein (Fragment).
 DS Hepatitis B virus.
 SC Hepatitis B virus.
 DC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
 DX NCBI_TaxID=10407;
 XN [1]
 XP SEQUENCE FROM N.A.
 RC STRAIN=23;
 TX PubMed=12185284;
 YA Hou J., Lin Y., Waters J., Wang Z., Min J., Liao H., Jiang J.,
 ZH Chen J., Luo K., Karayiannis P.;
 XT "Detection and significance of a G1862T variant of hepatitis B virus
 RT in Chinese patients with fulminant hepatitis.";
 RL J. Gen. Virol. 83:2291-2298(2002).
 DR EMBL; AF495684; AAM34071.1; -.
 JR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 PT NON TER 1
 TQ SEQUENCE 31 AA; 3380 MW; A776BDF508DEA72 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 31;
 Best Local Similarity 100.0%; Pred.No. 0.062;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 EIRLKVFL 9
 | | | | |
 Db 3 EIRLKVFL 11

earch completed: December 23, 2003, 08:46:13
 ob time : 25.6 secs

Result No.	Query			ID	DB	Length	Match	Score	Description
	1	2	3						
1	41	100.0	9	2	US-08-468-279-3				Sequence 3, Appli
2	41	100.0	9	4	US-09-051-006-5				Sequence 5, Appli
3	41	100.0	24	6	5204446-1				Patent No. 5204446
4	41	100.0	24	6	5204446-3				Patent No. 5204446
5	41	100.0	37	2	US-08-319-376-5				Sequence 5, Appli
6	41	100.0	153	6	5196194-20				Patent No. 5196194
7	41	100.0	153	6	5204446-4				Patent No. 5204446
8	41	100.0	154	6	5183734-1				Patent No. 5183734
9	37	90.2	154	4	US-09-719-528A-5				Sequence 5, Appli
10	34	82.9	24	6	5204446-2				Patent No. 5204446
11	31	75.6	230	3	US-08-818-112-65				Sequence 65, Appl
12	31	75.6	230	4	US-08-818-111-86				Sequence 66, Appl
13	31	75.6	230	4	US-09-058-536-65				Sequence 66, Appl
14	31	75.6	230	4	US-09-072-596-66				Sequence 66, Appl
15	30	73.2	540	4	US-09-107-532A-5314				Sequence 5314, Ap
16	30	73.2	848	4	US-09-259-991A-32257				Sequence 32257, A
17	29	70.7	30	2	US-08-934-915-186				Sequence 186, App
18	29	70.7	228	3	US-08-569-221A-2				Sequence 2, Appli
19	29	70.7	596	4	US-09-259-991A-26031				Sequence 26031, A
20	29	70.7	647	4	US-09-259-991A-26052				Sequence 26052, A
21	29	70.7	1408	1	US-08-613-531-2				Sequence 2, Appli
22	28	68.3	233	4	US-09-214-631-7				Sequence 7, Appli
23	28	68.3	234	1	US-08-299-567-5				Sequence 5, Appli
24	28	68.3	238	1	US-08-240-124-2				Sequence 2, Appli
25	28	68.3	238	1	US-08-453-943-2				Sequence 2, Appli
26	28	68.3	238	2	US-09-057-121-2				Sequence 2, Appli
27	28	68.3	238	3	US-09-358-734-2				Sequence 2, Appli

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; Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 EIRLKFVFL 9
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Db 1 EIRLKFVFL 9

RESULT 2
US-09-051-006-5
; Sequence 5, Application US/09051006
; Patent No. 6380359
; GENERAL INFORMATION:
; APPLICANT: Mogam Biotechnology Research Institute
; APPLICANT: Kim, Tae-Young
; APPLICANT: Lee, Ki-Young
; APPLICANT: Chang, Jin-Soo
; APPLICANT: Cho, Sung-Yoo
; APPLICANT: Hwang, Yu-Kyeong
; APPLICANT: Choi, Myeong
; APPLICANT: Cheong, Hong-Seok
; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
; FILE REFERENCE: 0136/08154
; CURRENT APPLICATION NUMBER: US/09/051,006
; CURRENT FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-051-006-5

Query Match 100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 EIRLKFVFL 9
   |||||
Db 1 EIRLKFVFL 9

RESULT 3
5204446-1
; Patent No. 5204446
; APPLICANT: KUMAZAWA, TOSHIKI;OSANAI, MASATOSHI
; TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY
; WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/503,239
; FILING DATE: 02-APR-1990
; SEQ ID NO:1
; LENGTH: 24
5204446-1

Query Match 100.0%; Score 41; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.03; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 EIRLKFVFL 9
   |||||
Db 13 EIRLKFVFL 21

RESULT 4
5204446-3
; Patent No. 5204446
; APPLICANT: KUMAZAWA, TOSHIKI;OSANAI, MASATOSHI
; TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY
; WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS
; NUMBER OF SEQUENCES: 4
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/503,239
; FILING DATE: 02-APR-1990
; SEQ ID NO:3
; LENGTH: 24
5204446-3

Query Match 100.0%; Score 41; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.03; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 EIRLKFVFL 9
   |||||
Db 13 EIRLKFVFL 21

RESULT 5
US-08-319-376-5
; Sequence 5, Application US/08319376
; Patent No. 5872286
; GENERAL INFORMATION:
; APPLICANT: Liang, Tsanyang J
; APPLICANT: Huang, Jiakang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INTERFERING
; WITH HEPATITIS B VIRUS INFECTION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,376
; FILING DATE: 06-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Ph.D., Kathleen A.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: MGH-126XX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-319-376-5

Query Match 100.0%; Score 41; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.046; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 EIRLKFVFL 9
   |||||
Db 16 EIRLKFVFL 24

RESULT 6
5196194-20
; Patent No. 5196194
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APPLICANT: RUTTER, WILLIAM J.; GOODMAN, HOWARD M.
TITLE OF INVENTION: VACCINES CONTAINING HEPATITIS B S-PROTEIN
NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/679,621
FILING DATE: 7-DEC-1984
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 513,055
FILING DATE: 12-JUL-1983
APPLICATION NUMBER: 107,267
FILING DATE: 21-DEC-1979
APPLICATION NUMBER: 41,909
FILING DATE: 24-MAY-1979
SEQ ID NO: 20:
LENGTH: 153
5196194-20

Query Match 100.0%; Score 41; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 126 EIRLKVFL 134

RESULT 7
5204446-4
Patent No. 5204446
APPLICANT: KUMAZAWA, TOSHIKI; OSANAI, MASATOSHI
TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY
WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/503,239
FILING DATE: 02-APR-1990
SEQ ID NO: 4:
LENGTH: 153
5204446-4

Query Match 100.0%; Score 41; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 125 EIRLKVFL 133

RESULT 8
5183734-1
Patent No. 5183734
APPLICANT: MORIARTY, ANN M.
TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
FOR ASSAYING SV40 HBXAG
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,982
FILING DATE: 17-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 54,424
FILING DATE: 26-MAY-1987
APPLICATION NUMBER: 648,142
FILING DATE: 07-SEP-1984
APPLICATION NUMBER: 587,570
FILING DATE: 08-MAR-1984
SEQ ID NO: 1:
LENGTH: 154
5183734-1

Query Match 100.0%; Score 41; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 126 EIRLKVFL 134

RESULT 9
US-09-719-528A-5
Sequence 5, Application US/09719528A
Patent No. 6558675
GENERAL INFORMATION:
APPLICANT: Oon, Chong Jin
Lim, Gek Keow
Zhao, Yi
Chen, Wei Ning
TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
USES THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ladas & Parry
STREET: 26 West 61 Street
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10023
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/719,528A
FILING DATE: 30-APR-2001
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SG98/00046
FILING DATE: 19-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Mass, Clifford J.
REGISTRATION NUMBER: 30,086
REFERENCE/DOCKET NUMBER: U-013109-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 708-1800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-719-528A-5

Query Match 90.2%; Score 37; DB 4; Length 154;
Best Local Similarity 77.8%; Pred. No. 1.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 126 EIRLKVFL 134

RESULT 10
5204446-2
Patent No. 5204446
APPLICANT: KUMAZAWA, TOSHIKI; OSANAI, MASATOSHI
TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY
WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/503,239
FILING DATE: 02-APR-1990
SEQ ID NO: 2:
LENGTH: 24

5204446-2

Query Match 82.9%; Score 34; DB 6; Length 24;
Best Local Similarity 77.8%; Pred. No. 0.91;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKVFVL 9
|||:|
Db 13 EIRLMIFVL 21

RESULT 11

US-08-818-112-65
; Sequence 65, Application US/08818112
; Patent No. 6290969
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 13-MAR-1997
; APPLICATION NUMBER: US/08/818,112
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.41106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-818-112-65
; Sequence 65, Application US/08818112
; Patent No. 6290969
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 13-MAR-1997
; APPLICATION NUMBER: US/08/818,112
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.41106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

Query Match 75.6%; Score 31; DB 3; Length 230;
Best Local Similarity 44.4%; Pred. No. 37;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFVL 9
|||:|
Db 66 DVRKIFVL 74

RESULT 12

US-08-818-111-66
; Sequence 66, Application US/08818111
; Patent No. 6338852
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 13-MAR-1997
; APPLICATION NUMBER: US/08/818,111
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-818-111-66

Query Match 75.6%; Score 31; DB 4; Length 230;
Best Local Similarity 44.4%; Pred. No. 37;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFVL 9
|||:|
Db 66 DVRKIFVL 74

RESULT 13

US-09-056-556-65
; Sequence 65, Application US/09056556
; Patent No. 6350456
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-APR-1998
; CLASSIFICATION:

TREAT

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.457
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-056-556-65

Query Match 75.6%; Score 31; DB 4; Length 230;
Best Local Similarity 44.4%; Pred. No. 37;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFVL 9
DB 66 DVRKIFML 74

RESULT 14
US-09-072-596-66
; Sequence 66, Application US/09072596
; Patent No. 6438366
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonia
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Hardrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 350
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,596
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-072-596-66

Query Match 75.6%; Score 31; DB 4; Length 230;
Best Local Similarity 44.4%; Pred. No. 37;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFVL 9
DB 66 DVRKIFML 74

RESULT 15
US-09-107-532A-5314
; Sequence 5314, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 893-5007
; TELEFAX: (781) 893-8277
; INFORMATION FOR SEQ ID NO: 5314:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...540
; SEQUENCE DESCRIPTION: SEQ ID NO: 5314:
; US-09-107-532A-5314

Query Match 73.2%; Score 30; DB 4; Length 540;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVF 7
DB 440 EIRLKLF 446

Search completed: December 23, 2003, 08:53:52
Job time : 11.6 secs
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 6.4 Seconds
(without alignments)

66.131 Million cell updates/sec

Title: US-09-989-621-1

Perfect score: 45

Sequence: 1 HLSIRGLFV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	154	1 X HPEV4	P12336 hepatitis b
2	37	82.2	1436	1 WC11_BOVIN	P30205 bos taurus
3	35	77.8	154	1 X HPEV2	P30166 hepatitis b
4	35	77.8	154	1 X HPEV9	P17102 hepatitis b
5	35	77.8	154	1 X HPEV4	P24026 hepatitis b
6	35	77.8	154	1 X HPEV1	P20375 hepatitis b
7	35	77.8	154	1 X HPEVJ	P20376 hepatitis b
8	35	77.8	154	1 X HPEVL	P12912 hepatitis b
9	35	77.8	154	1 X HPEVO	P20977 hepatitis b
10	35	77.8	154	1 X HPEVT	Q05499 hepatitis b
11	35	77.8	154	1 X HPEVY	P30165 hepatitis b
12	34	75.6	178	1 P20K_CLOPA	P23161 clostridium
13	34	75.6	361	1 P2Z8_METTF	P29585 methanobact
14	33	73.3	256	1 PDX3_HUMAN	P30048 homo sapien
15	33	73.3	257	1 PDX3_BOVIN	P35705 bos taurus
16	33	73.3	695	1 TKT2_RHIME	P56900 rhizobium m
17	32	71.1	369	1 PYRD_DEIRA	Q9rx14 deinococcus
18	32	71.1	430	1 YJCF_ECOLI	P32704 escherichia
19	32	71.1	628	1 YS9A_CABEL	Q960a0 caenorhabdi
20	32	71.1	870	1 POL_TSRV	P31423 sheep pulmo
21	32	71.1	1020	1 CARE_MOUSE	Q8k320 mus musculu
22	32	71.1	1884	1 RRP5_HUMAN	Q14690 homo sapien
23	32	71.1	4563	1 APB_HUMAN	P04114 homo sapien
24	31	68.9	193	1 TDX_ECHGR	Q8t6c4 echinococcu
25	31	68.9	195	1 TSA2_YEAST	Q04120 saccharomyc
26	31	68.9	200	1 Y755_SYNY3	Q56624 synecocyst
27	31	68.9	210	1 BAS1_HORVU	Q96468 hordeum vul
28	31	68.9	210	1 BAS1_WHEAT	P80602 triticum ae
29	31	68.9	257	1 PDX3_MOUSE	P20108 mus musculu
30	31	68.9	265	1 BAS1_SPIOL	Q24364 spinacia ol
31	31	68.9	266	1 BAS1_ARATH	Q96291 arabidopsis
32	31	68.9	361	1 Y439_METJA	Q57881 methanococc
33	31	68.9	361	1 YPVB_METTF	P29584 methanobact

ALIGNMENTS

RESULT 1

X HPEV4
ID X HPEV4 STANDARD; PRT; 154 AA.
AC P12935; 1992 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adr4).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10409;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83246570; PubMed=6306594;
RA Fujiyama A., Miyachara A., Nozaki C., Yoneyama T., Ohtomo N.,
RA Matsubara K.;
RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype
RT adr.";
RL Nucleic Acids Res. 11:4601-4610(1983).
CC -1- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
CC
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CC
CC EMBL; X01587; CAA25744.1; -
CC InterPro; IPR000236; TransactX.
CC Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16622 MW; 594A1D0718928804 CRC64;

Query Match 100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSIRGLFV 9

DB 52 HLSIRGLFV 60

RESULT 2

WC11_BOVIN
ID WC11_BOVIN STANDARD; PRT; 1436 AA.
AC P30205;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen WC1.1 precursor.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.

NCBI_TaxID=9913;
 [1] X_HPBV2 STANDARD; PRT; 154 AA.
 AC P03166; P12935;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Trans-activating protein X.
 GN X.
 OS Hepatitis B virus (subtype adw2), and
 OS Hepatitis B virus (subtype adw).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OC NCBI_TaxID=10408, 106821;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ADW2;
 RC Valenzuela P., Quiroga M., Zaidivar J., Gray P., Rutter W.J.;
 RL (in) Field B.N., Jaenisch R., Fox C.P. (eds.);
 RL Animal virus genetics, pp.57-70, Academic Press, New York (1980).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ADW;
 RC MEDLINE=89045656; PubMed=3188399;
 RA Lo S.J., Chien M.L., Lee Y.H.W.;
 RT "Characteristics of the X gene of hepatitis B virus";
 RL Virology 167:289-292(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ADW;
 RC MEDLINE=83168919; PubMed=6300776;
 RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;
 RT "The complete nucleotide sequences of the cloned hepatitis B virus
 RT DNA; subtype adr and adw";
 RL Nucleic Acids Res. 11:1747-1757(1983).
 CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL; X02763; CA226540.1; -;
 CC EMBL; Z35717; CA84789.1; -;
 CC EMBL; M23692; AA56820.1; -;
 CC EMBL; V00866; -; NOT_ANNOTATED_CDS.
 CC FIR; A31283; QQVLAW.
 CC FIR; S47408; S47408.
 CC InterPro: IPR000236; TransactX.
 CC Pfam: PF00739; X; 1; 80 E -> A (IN REF. 3).
 CC CONFLICT 80 80
 CC CONFLICT 115 115 C -> S (IN REF. 2).
 CC FT CONFLICT 130 131 KV -> MI (IN REF. 3).
 CC SQ SEQUENCE 154 AA; 16993 MW; 7F2AE32A4F025670 CRC64;
 Query Match 77.8%; Score 35; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HSLRGL 7
 Db 52 HSLRGL 58
 RESULT 4
 X_HPBV9 STANDARD; PRT; 154 AA.
 AC F17102;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Trans-activating protein X.

NCBI_TaxID=9913;
 [1] X_HPBV2 STANDARD; PRT; 154 AA.
 AC P03166; P12935;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Trans-activating protein X.
 GN X.
 OS Hepatitis B virus (subtype adw2), and
 OS Hepatitis B virus (subtype adw).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OC NCBI_TaxID=10408, 106821;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ADW2;
 RC Valenzuela P., Quiroga M., Zaidivar J., Gray P., Rutter W.J.;
 RL (in) Field B.N., Jaenisch R., Fox C.P. (eds.);
 RL Animal virus genetics, pp.57-70, Academic Press, New York (1980).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ADW;
 RC MEDLINE=89045656; PubMed=3188399;
 RA Lo S.J., Chien M.L., Lee Y.H.W.;
 RT "Characteristics of the X gene of hepatitis B virus";
 RL Virology 167:289-292(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ADW;
 RC MEDLINE=83168919; PubMed=6300776;
 RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;
 RT "The complete nucleotide sequences of the cloned hepatitis B virus
 RT DNA; subtype adr and adw";
 RL Nucleic Acids Res. 11:1747-1757(1983).
 CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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 CC -----
 CC EMBL; X02763; CA226540.1; -;
 CC EMBL; Z35717; CA84789.1; -;
 CC EMBL; M23692; AA56820.1; -;
 CC EMBL; V00866; -; NOT_ANNOTATED_CDS.
 CC FIR; A31283; QQVLAW.
 CC FIR; S47408; S47408.
 CC InterPro: IPR000236; TransactX.
 CC Pfam: PF00739; X; 1; 80 E -> A (IN REF. 3).
 CC CONFLICT 80 80
 CC CONFLICT 115 115 C -> S (IN REF. 2).
 CC FT CONFLICT 130 131 KV -> MI (IN REF. 3).
 CC SQ SEQUENCE 154 AA; 16993 MW; 7F2AE32A4F025670 CRC64;
 Query Match 77.8%; Score 35; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HSLRGL 7
 Db 52 HSLRGL 58
 RESULT 4
 X_HPBV9 STANDARD; PRT; 154 AA.
 AC F17102;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Trans-activating protein X.

```

GN X. Hepatitis B virus (subtype adv / strain 991).
OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10410;
RN [1]
RR SEQUENCE FROM N.A.
RA Koehn H.G., Schuler A., Lottmann S., Thomsen R.;
RL submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
CC -----
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CC -----
CC EMBL; X51970; CAA36231.1; -
CC PIR; S10380; QOVLSK.
CC InterPro; IPR000236; TransactX.
CC Pfam; PF00739; X; 1.
CC SEQUENCE 154 AA; 16553 MW; 52A0D9CFE6DCE0 CRC64;
CC -----
CC Query Match 77.8%; Score 35; DB 1; Length 154;
CC Best Local Similarity 100.0%; Pred. No. 2.2;
CC Matches 7; Conservative 0; Mismatches 0; Gaps 0;
CC -----
CC 1 HLSLRL 7
CC 52 HLSLRL 58
CC -----
RR RESULT 5
RR X_HPBVA STANDARD; PRT; 154 AA.
RR AC P24026;
RR DT 01-MAR-1992 (Rel. 21, Created)
RR DT 01-MAR-1992 (Rel. 21, Last sequence update)
RR DT 01-NOV-1995 (Rel. 32, Last annotation update)
RR DE Trans-activating protein X.
RR GN X.
RR OS Hepatitis B virus (strain alpha).
RR OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
RR OX NCBI_TaxID=10411;
RR RN [1]
RR SEQUENCE FROM N.A.
RR MEDLINE=90266476; PubMed=2345966;
RR Tong S., Li J., Vitvitski L., Trepo C.;
RR "Active hepatitis B virus replication in the presence of anti-HBe is
RR associated with viral variants containing an inactive pre-C region.";
RR Virolgy 176:596-603(1990).
RR -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
RR -----
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RR -----
RR EMBL; M32138; AAA45504.1; -
RR PIR; D34773; QOVLSA.
RR InterPro; IPR000236; TransactX.
RR Pfam; PF00739; X; 1.
RR SEQUENCE 154 AA; 16671 MW; 2CFEA77FA5E271F CRC64;
RR -----
RR Query Match 77.8%; Score 35; DB 1; Length 154;
RR Best Local Similarity 100.0%; Pred. No. 2.2;
RR Matches 7; Conservative 0; Mismatches 0; Gaps 0;
RR -----
RR 1 HLSLRL 7

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Db 52 HLSLRL 58
RESULT 6
X_HPBVI STANDARD; PRT; 154 AA.
AC P20975;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adv / strain Indonesia/pIDW420).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10412;
OX [1]
RR SEQUENCE FROM N.A.
RR MEDLINE=89010694; PubMed=3171552;
RR Okamoto H., Tsuda F., Sakugawa H., Sastrosowigno R.I., Imai M.,
RR Miyakawa Y., Mayumi M.;
RR "Typing hepatitis B virus by homology in nucleotide sequence:
RR comparison of surface antigen subtypes.";
RR J. Gen. Virol. 69:2575-2583(1988).
RR -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
RR -----
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RR -----
RR EMBL; D00331; -; NOT_ANNOTATED_CDS.
RR PIR; JS0604; JS0604.
RR InterPro; IPR000236; TransactX.
RR Pfam; PF00739; X; 1.
RR SEQUENCE 154 AA; 16556 MW; C80C817E961BFFB9 CRC64;
RR -----
RR Query Match 77.8%; Score 35; DB 1; Length 154;
RR Best Local Similarity 100.0%; Pred. No. 2.2;
RR Matches 7; Conservative 0; Mismatches 0; Gaps 0;
RR -----
RR 1 HLSLRL 7
RR 52 HLSLRL 58
RR -----
RR RESULT 7
RR X_HPBVI STANDARD; PRT; 154 AA.
RR AC P20976;
RR DT 01-FEB-1991 (Rel. 17, Created)
RR DT 01-FEB-1991 (Rel. 17, Last sequence update)
RR DT 01-NOV-1995 (Rel. 32, Last annotation update)
RR DE Trans-activating protein X.
RR GN X.
RR OS Hepatitis B virus (subtype adv / strain Japan/pJW233).
RR OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
RR OX NCBI_TaxID=10413;
RR [1]
RR SEQUENCE FROM N.A.
RR MEDLINE=89010694; PubMed=3171552;
RR Okamoto H., Tsuda F., Sakugawa H., Sastrosowigno R.I., Imai M.,
RR Miyakawa Y., Mayumi M.;
RR "Typing hepatitis B virus by homology in nucleotide sequence:
RR comparison of surface antigen subtypes.";
RR J. Gen. Virol. 69:2575-2583(1988).
RR -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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CC -----
 DR EMBL; D00329; -; NOT_ANNOTATED_CDS.
 DR PIR; J50256; JS0256; TransactX.
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 DR Trans-activating protein X.
 SQ SEQUENCE 154 AA; 16585 MW; 512A5A077169D5CA CRC64;

Query Match 77.8%; Score 35; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred.No. 2.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSRGL 7
 |||||
 Db 52 HLSRGL 58

RESULT 8

X_HPBVL STANDARD; PRT; 154 AA.
 AC P12912;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Trans-activating protein X.
 GN X.
 OS Hepatitis B virus (strain Ish / chimpanzee isolate).
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10414;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88258473; PubMed=2838576;
 RA Vaadin M., Wolstenholme A.J., Tsiquaye K.N., Zuckerman A.J.,
 RA Harrison T.J.;
 RT "The complete nucleotide sequence of the genome of a hepatitis B
 RT virus isolated from a naturally infected chimpanzee."
 RL J. Gen. Virol. 69:1383-1389(1988).
 CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.

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CC -----
 DR EMBL; D00220; BAA00160.1; -;
 DR PIR; D28885; QQVLCF.
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 DR Trans-activating protein X.
 SQ SEQUENCE 154 AA; 16759 MW; F6C9D7D30C16D743 CRC64;

Query Match 77.8%; Score 35; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred.No. 2.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSRGL 7
 |||||
 Db 52 HLSRGL 58

RESULT 9

X_HPBVO STANDARD; PRT; 154 AA.
 AC P20977;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Trans-activating protein X.
 GN X.
 OS Hepatitis B virus (strain Ish / chimpanzee isolate).
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10414;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88258473; PubMed=2838576;
 RA Vaadin M., Wolstenholme A.J., Tsiquaye K.N., Zuckerman A.J.,
 RA Harrison T.J.;
 RT "The complete nucleotide sequence of the genome of a hepatitis B
 RT virus isolated from a naturally infected chimpanzee."
 RL J. Gen. Virol. 69:1383-1389(1988).
 CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.

DE Trans-activating protein X.
 GN X.
 OS Hepatitis B virus (subtype adw / strain Okinawa/PODW282).
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10415;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89010694; PubMed=3171552;
 RA Okamoto H., Tsuda F., Sakugawa H., Sastroewignjo R.I., Imai M.,
 RA Miyakawa Y., Mayumi M.;
 RT "Typing hepatitis B virus by homology in nucleotide sequence:
 RT comparison of surface antigen subtypes.";
 RL J. Gen. Virol. 69:2575-2583(1988).
 CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.

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CC -----
 DR EMBL; D00330; -; NOT_ANNOTATED_CDS.
 DR PIR; J50603; JS0603.
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 DR Trans-activating protein X.
 SQ SEQUENCE 154 AA; 16558 MW; E2646C059A30125F CRC64;

Query Match 77.8%; Score 35; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred.No. 2.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSRGL 7
 |||||
 Db 52 HLSRGL 58

RESULT 10

X_HPBVT STANDARD; PRT; 154 AA.
 AC Q05499;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Trans-activating protein X.
 GN X.
 OS Hepatitis B virus (subtype adw4 / strain Brazil / isolate w4B).
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=45410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93346970; PubMed=8345355;
 RA Naumann H., Schaefer S., Yoshida C.F.T., Gaspar A.M.C., Repp R.,
 RA Gerlich W.H.;
 RT "Identification of a new hepatitis B virus (HBV) genotype from Brazil
 RT that expresses HBV surface antigen subtype adw4.";
 RL J. Gen. Virol. 74:1627-1632(1993).
 CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.

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CC -----
 DR EMBL; X69798; CAA49453.1; -;
 DR PIR; J02228; J02228.
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 DR Trans-activating protein X.
 SQ SEQUENCE 154 AA; 16715 MW; B523C051B9B0B737 CRC64;

Query Match 77.8%; Score 35; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred. No. 2.2; 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSRGL 7
 DB 52 HLSRGL 58

RESULT 11

ID X_HPBVV STANDARD; PRT; 154 AA.

AC P03165;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Trans-activating protein X.
 GN X.
 OS Hepatitis B virus (subtype ayw).
 OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
 OC NCBI_TaxID=10418;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81012091; PubMed=399327;
 RA Galibert F., Mandart E., Piteussel F., Tiollais P., Charnay P.;
 RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)
 cloned in E. coli.";
 RL Nature 281:646-650(1979).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Latvia;
 RX MEDLINE=85204397; PubMed=3996597;
 RA Bichko V., Dreilina D., Pushko P.M., Pumpen P.P., Gren E.;
 RT "Subtype ayw variant of hepatitis B virus. DNA primary structure
 analysis.";
 RL FEBS Lett. 185:208-212(1985).
 RN [1]
 RP FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.

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EMBL; V01460; -; NOT ANNOTATED_CDS.
 EMBL; X02496; CAB41657.1; -;
 PIR; A03719; QOVLDI.
 PIR; A05237; QOVLBI.
 InterPro; IPR00236; TransactX.
 Pfam; PF00739; X; 1.
 T VARIANT 46 46 P -> S (IN STRAIN LATVIA).
 T VARIANT 84 88 NAHQI -> KAQPF (IN STRAIN LATVIA).
 T VARIANT 102 102 A -> V (IN STRAIN LATVIA).
 T CONFLICT 26 26 R -> C (IN REF. 1).
 Q SEQUENCE 154 AA; 16618 MW; 29FDLCSE09A34B5 CRC64;

Query Match 77.8%; Score 35; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 HLSRGL 7
 b 52 HLSRGL 58

RESULT 12

D 20X_CLOPA STANDARD; PRT; 178 AA.
 C P23161;
 T 01-NOV-1991 (Rel. 20, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 20 kDa protein in rubredoxin operon (ORF C).
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OC NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92344580; PubMed=1637309;
 RA Mathieu J., Meyer J., Moulis J.M.;
 RT "Cloning, sequencing and expression in Escherichia coli of the
 rubredoxin gene from Clostridium pasteurianum.";
 RL Biochem. J. 285:255-262(1992).
 CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
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EMBL; M60116; AAA23278.1; -;
 PIR; S29119; S29119.
 HSRP; P30041; IPRX.
 InterPro; IPR000866; Ahpc-TSA.
 Pfam; PF00578; Ahpc-TSA; 1.
 KW Oxidoreductase.
 FT ACT SITE 50 50 BY SIMILARITY.
 FT ACT SITE 167 167 BY SIMILARITY.
 SQ SEQUENCE 178 AA; 20036 MW; DP9AD3D8F1B93A64 CRC64;

Query Match 75.8%; Score 34; DB 1; Length 178;
 Best Local Similarity 75.0%; Pred. No. 4.2;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSLRGLFV 9
 DB 123 ISLRLGFI 130

RESULT 13

YP28 METTF STANDARD; PRT; 361 AA.
 ID YP28 METTF
 AC P29585;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE Hypothetical 40.6 kDa protein (ORF8').
 OS Methanobacterium thermoformicicum.
 OG Plasmid pFZ1.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OC NCBI_TaxID=145262;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 3720 / Z-245;
 RX MEDLINE=93126090; PubMed=1336177;
 RA Noelling J., van Eeden F.J.M., Eggen R.I.L., de Vos W.M.;
 RT "Modular organization of related Archaeal plasmids encoding different
 restriction-modification systems in Methanobacterium
 thermoformicicum.";
 RL Nucleic Acids Res. 20:6501-6507(1992).
 CC -1- SIMILARITY: TO THE CORRESPONDING ORF IN PFV1.
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CC      -----
CC      EMBL: X68367; CAA48439.1; -.
CC      PIR: S30325; S30325.
CC      KW Hypothetical protein; Plasmid.
CC      SQ SEQUENCE 361 AA; 40565 MW; 5787C9D090AG384P CRC64;
CC
CC      Query Match 75.6%; Score 34; DB 1; Length 361;
CC      Best Local Similarity 87.5%; Pred. No. 8.7;
CC      Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC
CC      Qy 1 HSLRGLFV 8
CC      |||||
CC      Db 223 HSLRGLFV 230
CC
CC      RESULT 14
CC      ID PDX3_HUMAN STANDARD; PRT; 256 AA.
CC      AC P30048; P35690; Q13776; Q96HK4;
CC      DT 01-APR-1993 (Rel. 25, Created)
CC      DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC      DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC      DE Thioredoxin-dependent peroxide reductase, mitochondrial precursor
CC      DE (EC 1.1.1.1.-) (Peroxiredoxin 3) (Antioxidant protein 1) (AOP-1) (MERS
CC      DE protein homolog) (HBC189) (PRX III).
CC      GN PRDX3 OR AOP1
CC      OS Homo sapiens (Human).
CC      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CC      OX NCBI_TaxID=9606;
CC      [1]
CC      RP SEQUENCE FROM N.A.
CC      RC TISSUE=Blood;
CC      RX MEDLINE=9251598; PubMed=7733872;
CC      RA Teuji K., Copeland N.G., Jenkins N.A., Obinata M.;
CC      RA "Mammalian antioxidant protein complements alkylhydroperoxide
CC      RA reductase (ahpC) mutation in Escherichia coli.";
CC      RL Biochem. J. 307:377-381(1995).
CC      [2]
CC      RP SEQUENCE FROM N.A.
CC      RC TISSUE=Skin, Testis, Urinary bladder, and Uterus;
CC      RX MEDLINE=22388257; PubMed=12477932;
CC      RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
CC      RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
CC      RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
CC      RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
CC      RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
CC      RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
CC      RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
CC      RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
CC      RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
CC      RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
CC      RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
CC      RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
CC      RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
CC      RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC      RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
CC      RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smallos D.E.,
CC      RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
CC      RA "Generation and initial analysis of more than 15,000 full-length
CC      RA human and mouse cDNA sequences.";
CC      RP Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC      [3]
CC      RP SEQUENCE OF 148-240 FROM N.A.
CC      RX MEDLINE=94108427; PubMed=7506601;
CC      RA Takeda J., Yano H., Eng S., Zeng Y., Bell G.I.;
CC      RA "A molecular inventory of human pancreatic islets: sequence analysis
CC      RA of 1000 cDNA clones.";
CC      RP Hum. Mol. Genet. 2:1793-1798(1993).
CC      [4]
CC      RP SEQUENCE OF 63-72.
CC      RP TISSUE=Liver;

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```

RX MEDLINE=93162045; PubMed=1286669;
RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
RA Pasquali C., Sanchez J.-C., Tisot J.-D., Bjellqvist B., Vargas R.,
RA Appel R.D., Hughes G.J.;
RT "Human liver protein map: a reference database established by
RT microsequencing and gel comparison.";
RL Electrophoresis 13:992-1001(1992).
RN [5]
RP OVEROXIDATION OF CYS-108.
RX MEDLINE=22201787; PubMed=12059788;
RA Wagner E., Lucie S., Penna L., Chevallet M., van Dorsselaer A.,
RA Leize-Wagner E., Rabilloud T.;
RT "A method for detection of overoxidation of cysteines: peroxiredoxins
RT are oxidized in vivo at the active-site cysteine during oxidative
RT stress.";
RL Biochem. J. 366:777-785(2002).
CC -!- FUNCTION: Involved in redox regulation of the cell. Protects
CC radical-sensitive enzymes from oxidative damage by a radical-
CC generating system.
CC -!- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- MISCELLANEOUS: The active site is the redox-active Cys-108
CC oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-229-SH of the
CC other subunit to form an intermolecular disulfide with a
CC concomitant homodimer formation. The enzyme may be subsequently
CC regenerated by reduction of the disulfide by thioredoxin.
CC -!- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-108
CC (to Cys-SO3H) upon oxidative stress.
CC -!- SIMILARITY: BELONGS TO THE AHP/TSA FAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL: D49396; BAA08389.1; -.
CC EMBL: BC002685; AAH02685.1; -.
CC EMBL: BC008038; AAH08038.1; -.
CC EMBL: BC008435; AAH08435.1; -.
CC EMBL: BC021691; AAH21691.1; -.
CC EMBL: BC022373; AAH22373.1; -.
CC EMBL: T10952; -. NOT ANNOTATED_CDS.
CC SWISS-2DPAGE: P30048; HUMAN.
CC Sigena-2DPAGE: P30048; -.
CC Genew; HGNC:9354; PRDX3.
CC MIN; 604769; -.
CC GO; GO:0008785; F:alkyl hydroperoxide reductase activity; TAS.
CC InterPro; IPR000866; AhpC-TSA.
CC Pfam; PF00578; AhpC-TSA; 1.
CC Antioxidant; Peroxidase; Oxidoreductase; Redox-active center;
CC Mitochondrion; Transit peptide.
CC TRANSIT 1 62 MITOCHONDRION.
CC CHAIN 63 256 THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE.
CC ACT_SITE 108 108 CYSTEINE SULFENIC ACID INTERMEDIATE
CC (BY SIMILARITY)
CC DISULFID 108 108 INTERCHAIN (WITH C-229) (IN
CC LINKED FORM) (BY SIMILARITY).
CC DISULFID 229 229 INTERCHAIN (WITH C-108) (IN
CC LINKED FORM) (BY SIMILARITY).
CC CONFLICT 31 31 R -> W (IN REF. 2; AAH08435).
CC SEQUENCE 256 AA; 27692 MW; 8BB7F5E55BFE9BE CRC64;
CC
CC Query Match 73.3%; Score 33; DB 1; Length 256;
CC Best Local Similarity 75.0%; Pred. No. 10;
CC Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CC
CC Qy 2 LSLRGLFV 9
CC |||||
CC Db 181 LALRGLFI 188

```

RESULT 15
D PDX3_BOVIN STANDARD; PRT; 257 AA.
C C P35705;
T 01-JUN-1994 (Rel. 29, Created)
T 01-NOV-1997 (Rel. 35, Last sequence update)
T 15-SEP-2003 (Rel. 42, Last annotation update)
E Thioredoxin-dependent peroxidase reductase, mitochondrial precursor
E (EC 1.1.1.1.-) (Peroxiredoxin 3) (Antioxidant protein 1) (AOP-1) (SP-22
E protein).
S Bos taurus (Bovine).
S Bos taurus (Bovine).
S Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
S Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
S Bovidae; Bovinae; Bos.
S NCBI_TaxID=9913;
N [1]
N SEQUENCE FROM N.A.
N TISSUE=Adrenal medulla;
P MEDLINE=97069947; PubMed=8912927;
C Hiroi T., Watabe S., Takimoto K., Yago N., Yamoto Y., Takahashi S.Y.;
X "The cDNA sequence encoding bovine SP-22, a new defence system
T against reactive oxygen species in mitochondria.";
L DNA Seq. 5:239-242(1996).
L [2]
P SEQUENCE OF 2-257 FROM N.A.
P TISSUE=Adrenal medulla;
C MEDLINE=94375407; PubMed=8089078;
X Watabe S., Kohno H., Kouyama H., Hiroi T., Yago N., Nakazawa T.;
A "Purification and characterization of a substrate protein for
T mitochondrial ATP-dependent protease in bovine adrenal cortex.";
L J. Biochem. 115:648-654(1994).
L -!- FUNCTION: Involved in redox regulation of the cell. Protects
C radical-sensitive enzymes from oxidative damage by a radical-
C generating system.
C -!- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By
C similarity).
C -!- SUBCELLULAR LOCATION: Mitochondrial.
C -!- MISCELLANEOUS: The active site is the redox-active Cys-109
A oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-230-SH of the
T other subunit to form an intermolecular disulfide with a
L concomitant homodimer formation. The enzyme may be subsequently
C regenerated by reduction of the disulfide by thioredoxin (By
C similarity).
C -!- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-109
C (to Cys-SO3H) upon oxidative stress (By similarity).
C -!- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.

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between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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or send an email to license@sib-sib.ch).

EMBL; D82025; BAA11511.1; -
HSSP; P30041; 1PRX.
InterPro; IPR000866; Ahpc-TSA.
Pfam; PF00578; Ahpc-TSA; 1.
Antioxidant; Peroxidase; Oxidoreductase; Redox-active center;
Mitochondrion; Transit peptide.
TRANSIT 1 63
CHAIN 64 257
ACT_SITE 109 109
DISULFID 109 109
DISULFID 230 230
SEQUENCE 257 AA; 28195 MW; P2E89EE2F172A42D CRC64;
MITOCHONDRION (BY SIMILARITY).
THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE.
CYSTEINE SULFENIC ACID INTERMEDIATE
(BY SIMILARITY).
INTERCHAIN (WITH C-230) (IN
LINKED FORM) (BY SIMILARITY).
INTERCHAIN (WITH C-109) (IN
LINKED FORM) (BY SIMILARITY).

Query Match 73.3%; Score 33; DB 1; Length 257;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSLRGLFV 9
|:|||||:
Db 182 LALRGLFI 189

Search completed: December 23, 2003, 08:41:44
Job time : 9.4 secs

GenCore version 5.1.6
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M protein - protein search, using sw model

run on: December 23, 2003, 08:39:57, Search time 25.8 Seconds
(without alignments)
55,370 Million cell updates/sec

title: US-09-989-621-3

effect score: 42

sequence: 1 AMSTTDLEA 9

coring table: BLOSUM62
Gapop 10.0, Gapext 0.5

sarched: 1107863 seqs, 158726573 residues

total number of hits satisfying chosen parameters: 1107863

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atadase :

A_Geneseq_19Jun03.*

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2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
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13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
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19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	42	100.0	9	20	Hepatitis B virus
2	42	100.0	9	23	Hepatitis B virus
3	42	100.0	9	23	Hepatitis B virus
4	42	100.0	15	6	Sequence of an ant
5	42	100.0	15	23	Hepatitis B virus
6	42	100.0	15	23	Hepatitis B virus
7	42	100.0	16	9	Antigenic determin
8	42	100.0	134	16	Hepatitis B virus
9	42	100.0	154	6	Sequence of the an

10	42	100.0	154	9	AAPE2174	Peptide encoded by
11	42	100.0	154	21	AAV58473	Hepatitis B virus
12	42	100.0	154	21	AAV54047	Amino acid seque
13	42	100.0	154	21	AAV44351	Human hepatitis B
14	38	90.5	8	23	ABJ07178	Hepatitis B virus
15	38	90.5	8	23	ABJ08117	Hepatitis B virus
16	38	90.5	9	15	AAV38029	Hepatitis B virus
17	38	90.5	9	20	AAV45599	Immunogenic peptid
18	38	90.5	9	21	AAV73060	Hepatitis B virus
19	38	90.5	9	22	AAJ02041	Hepatitis C virus
20	38	90.5	9	23	ABJ05903	Hepatitis B virus
21	38	90.5	9	23	ABJ07244	Hepatitis B virus
22	38	90.5	9	23	ABJ07856	Hepatitis B virus
23	38	90.5	9	23	ABJ08118	Hepatitis B virus
24	38	90.5	9	23	ABJ08480	Hepatitis B virus
25	38	90.5	9	23	ABJ08831	Hepatitis B virus
26	38	90.5	9	23	ABJ09123	Hepatitis B virus
27	38	90.5	9	23	ABJ09849	Hepatitis B virus
28	38	90.5	10	23	ABJ07301	Hepatitis B virus
29	38	90.5	10	23	ABJ08119	Hepatitis B virus
30	38	90.5	11	23	ABJ06438	Hepatitis B virus
31	38	90.5	11	23	ABJ08120	Hepatitis B virus
32	38	90.5	11	23	ABJ08481	Hepatitis B virus
33	36	85.7	9	23	ABJ07696	Hepatitis B virus
34	34	81.0	7	23	ABJ05904	Hepatitis B virus
35	33	78.6	8	22	AAJ02048	Hepatitis B virus
36	33	78.6	8	23	ABJ05935	Hepatitis B virus
37	33	78.6	8	23	ABJ06836	Hepatitis B virus
38	33	78.6	8	23	ABJ07197	Hepatitis B virus
39	33	78.6	8	23	ABJ07863	Hepatitis B virus
40	33	78.6	8	23	ABJ08243	Hepatitis B virus
41	33	78.6	8	23	ABJ08547	Hepatitis B virus
42	33	78.6	9	23	ABJ05936	Hepatitis B virus
43	33	78.6	9	23	ABJ06837	Hepatitis B virus
44	33	78.6	9	23	ABJ07260	Hepatitis B virus
45	33	78.6	9	23	ABJ08244	Hepatitis B virus

ALIGNMENTS

RESULT 1

AAV24461

ID AAV24461 standard; peptide; 9 AA.

XX AC AAV24461;

XX DT 23-SEP-1999 (first entry)

XX DE Hepatitis B virus X protein peptide #3.

XX KW Hepatitis B virus; HBV; X protein; cytotoxic T lymphocyte; liposome; CTL; antigen; immunity; liver cancer.

XX OS Hepatitis B virus.

XX OS Synthetic.

XX PN WO9936434-A1.

XX PD 22-JUL-1999.

XX PF 19-JAN-1998; 98WO-KR00010.

XX PR 19-JAN-1998; 98WO-KR00010.

XX PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.

XX PI Chang J, Cheong H, Cho S, Choi M, Hwang Y, Kim T, Lee K;

XX DR WPI; 1999-444387/37.

XX PT Hepatitis B virus protein X-derived peptide antigens used to

PT Stimulate cytotoxic T lymphocytes, useful for treatment of
 XX HBV-associated diseases, especially liver cancer
 XX Claim 3; Page 24; 33pp; English.

CC The present invention describes peptide antigens AAY24459 to AAY24463
 CC derived from the X protein of hepatitis B virus (HBV) which are
 CC recognized by cytotoxic T lymphocytes (CTL). The peptide antigens
 CC derived from HBV X protein are useful for inducing CTLs against the
 CC virus or inducing immunological tolerance to the virus. pH-sensitive
 CC liposomes containing the peptide antigens are used to induce cellular
 CC immunity so that CTLs specific to the virus can be produced. This is
 CC useful for prevention and treatment of HBV-associated diseases,
 CC especially HBV-associated liver cancer. pH-sensitive liposomes permit
 CC the selective transportation of anti-cancer drugs.

XX Sequence 9 AA;

Query Match 100.0%; Score 42; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

NY 1 AMSTTDLEA 9
 DB 1 AMSTTDLEA 9

RESULT 2
 ABJ05975
 ID ABJ05975 standard; Peptide; 9 AA.

AC ABJ05975;
 DT 14-NOV-2002 (first entry)

DE Hepatitis B virus epitope #193.

GW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 GW virucide; hepatotropic; antiinflammatory.

OS Hepatitis B virus.

WN WO200219986-A1.

DD 14-MAR-2002.

FF 08-SEP-2000; 2000WO-US24802.

RR 08-SEP-2000; 2000WO-US24802.

AA (EPIM-) EPIMUNE INC.
 AA (SETT/) SETTE A.

II Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 II Celis E, Kubo RT, Grey HM, Chesnut RW;

RR WPI; 2002-643192/69.

TT Vaccine composition for treating or preventing hepatitis B virus (HBV)
 TT infection, and/or for stimulating an immune response to HBV, comprises
 TT a HBV peptide epitope -

SS Disclosure; Page 113; 228pp; English.

XX The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 42; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 DB 1 AMSTTDLEA 9

RESULT 3

ID ABJ07513 standard; Peptide; 9 AA.

AC ABJ07513;

DT 14-NOV-2002 (first entry)

DE Hepatitis B virus epitope #1731.

XX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 XX virucide; hepatotropic; antiinflammatory.

OS Hepatitis B virus.

PN WO200219986-A1.

PD 14-MAR-2002.

FF 08-SEP-2000; 2000WO-US24802.

RR 08-SEP-2000; 2000WO-US24802.

AA (EPIM-) EPIMUNE INC.
 AA (SETT/) SETTE A.

PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 PI Celis E, Kubo RT, Grey HM, Chesnut RW;

RR WPI; 2002-643192/69.

TT Vaccine composition for treating or preventing hepatitis B virus (HBV)
 TT infection, and/or for stimulating an immune response to HBV, comprises
 TT a HBV peptide epitope -

SS Disclosure; Page 145; 228pp; English.

CC The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 42; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 DB 1 AMSTTDLEA 9

RESULT 4

ID AAP50458 standard; Protein; 15 AA.

AC AAP50458;

DT 25-MAR-2003 (updated)

DT 27-SEP-1991 (first entry)

DE Sequence of an antigenic determinant of HBxAg, the antigen
 DE encoded by the X region of the hepatitis B virus genome.

Best Local Similarity 100.0%; Pred. No. 0.053; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 AMSTTDLEA 9
 |||||
 3 AMSTTDLEA 11

Db

RESULT 7
 AAP82170
 ID AAP82170 standard; protein; 16 AA.
 AC
 AAP82170;
 25-MAR-2003 (updated)
 06-JAN-1991 (first entry)
 Antigenic determinant of HBxAg.
 Antigenic peptide; HBxAg; antigenic polymer; assay; diagnosis;
 Hepatitis B virus.
 WO8809340-A.
 01-DEC-1988.
 24-MAY-1988; 88WO-US01719.
 26-MAY-1987; 87US-0054424.
 (SCRI) SCRIPPS CLINIC & RES FOUND.
 Moriarty AM;
 WPI; 1988-353925/49.
 Antigenic synthetic polypeptide(s) - contg. an amino acid sequence
 corresponding to an antigenic determinant of hepatitis B virus, HBxAg
 Claim 4; Page 90; 106pp; English.
 The peptide and antibodies reactive with it are used in diagnostic
 assays for HBxAg in a body sample. They can also be used in affinity
 matrices for isolation and purification.
 (Updated on 25-MAR-2003 to correct PA field.)
 Sequence 16 AA;
 Query Match 100.0%; Score 42; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.057;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 AMSTTDLEA 9
 |||||
 4 AMSTTDLEA 12

Db

RESULT 8
 AAR71563
 D AAR71563 standard; Protein; 134 AA.
 AC
 AAR71563;
 01-NOV-1995 (first entry)
 Hepatitis B virus polypeptide.
 Hepatitis B virus; PCR; amplification; primer; antiviral agent.
 Hepatitis B virus.
 JP07033797-A.

XX 03-FEB-1995.
 PD
 XX
 XX 21-JUL-1993; 93JP-0180314.
 PF
 XX
 XX 21-JUL-1993; 93JP-0180314.
 PR
 XX
 XX (MITU) MITSUBISHI KASEI CORP.
 PA
 XX
 XX WPI; 1995-110649/15.
 DR
 XX N-PSDB; AAQ85966.
 DR
 XX
 XX Polypeptide derived from hepatitis B virus and its coding gene.
 PT - may be used for detection of HBV not detectable by conventional
 PT methods
 XX
 XX
 PS Claim 1; Page 6; 7pp; Japanese.
 XX
 XX The amino acid sequence of a polypeptide derived from hepatitis B virus.
 CC The gene encoding this protein was derived from DNA isolated from
 CC patients infected with hepatitis virus which was not detected by
 CC conventional methods. The fragment encoding the polypeptide was
 CC subsequently PCR amplified using primers (AA085967-70). The polypeptide
 CC can be used in the diagnosis of hepatitis viral diseases which cannot be
 CC detected by conventional methods and in the development of antiviral
 CC agents.
 XX
 SQ Sequence 134 AA;
 Query Match 100.0%; Score 42; DB 16; Length 134;
 Best Local Similarity 100.0%; Pred. No. 0.54; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMSTTDLEA 9
 |||||
 Db 102 AMSTTDLEA 110

RESULT 9
 AAP50461
 ID AAP50461 standard; protein; 154 AA.
 AC
 AAP50461;
 25-MAR-2003 (updated)
 27-SEP-1991 (first entry)
 Sequence of the antigen HBxAg encoded by the X region of the
 hepatitis B virus genome.
 Hepatitis B virus; X region; antigen; diagnostic assay.
 Hepatitis B virus.
 Key Location/Qualifiers
 FH Region 23..154
 FT /note= "the substantial portion of HBxAg expressed
 FT by SVBHV-3. Ala (23) is the amino-terminal
 FT residue of the expressed HBxAg polypeptide"
 FT Peptide 100..115
 FT /label= Peptide 99
 FT Peptide 115..131
 FT /label= Peptide 100
 FT Peptide 144..154
 FT /label= Peptide 142
 XX
 XX WO8503950-A.
 DN
 XX
 XX 12-SEP-1985.
 PD
 XX
 XX 06-MAR-1985; 85WO-US00359.
 PF
 XX
 XX 07-SEP-1984; 84US-0648142.
 PR

R 08-MAR-1984; 84US-0587570.
 R 26-MAY-1987; 87US-0054424.
 X A (SCRI) SCRIPPS CLINIC & RES FOUND.
 X Moriarty AM, Alexander H, Lerner RA;
 R WPI; 1985-236420/38.
 R Expression vector contg. gene coding for hepatitis B HBxAg -
 T useful in diagnostic systems for detection of HBxAg and its
 T antibody in body samples
 S Disclosure; Fig 6; 86pp; English.
 X The inventors claim an antigenic synthetic polypeptide containing
 X about 6 to about 40 AA residues corresponding in AA residue sequence
 X to an antigenic determinant of HBxAg (see AAP50458-P50460). The
 X antigenic polypeptides may be used in a diagnostic assay system for
 X determining the presence of HBxAg in a body sample.
 X (Updated on 25-MAR-2003 to correct PF field.)
 X (Updated on 25-MAR-2003 to correct PA field.)
 X Q Sequence 154 AA;
 Query Match 100.0%; Score 42; DB 6; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.62; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;
 Y 1 AMSTTDLEA 9
 b 102 AMSTTDLEA 110
 RESULT 10
 AP82174
 D AAP82174 standard; protein; 154 AA.
 X AAP82174;
 25-MAR-2003 (updated)
 01-JAN-1980 (first entry)
 X Peptide encoded by HBxAg gene.
 X Antigenic peptide; HBxAg; antigenic polymer; assay; diagnosis;
 X Hepatitis B virus.
 X Key Location/Qualifiers
 X Region 23...0
 X Region /label=Portion of HbxAg expressed by SVBHV-3
 X Region 100..115
 X Region /label=Synthetic polypeptide 99
 X Region 115..131
 X Region /label=Synthetic polypeptide 100
 X Region 144..154
 X /label=Synthetic polypeptide 142
 X WO8809340-A.
 X 01-DEC-1988.
 X 24-MAY-1988; 88WO-US01719.
 X 26-MAY-1987; 87US-0054424.
 X (SCRI) SCRIPPS CLINIC & RES FOUND.
 X Moriarty AM;
 X WPI; 1988-353925/49.

PT Antigenic synthetic polypeptide(s) - contg. an amino acid sequence
 PT corresponding to an antigenic determinant of hepatitis B virus, HBxAg
 XX Disclosure; Fig. 6; 106pp; English.
 PS The polypeptide is encoded by the HbxAg gene.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX SQ Sequence 154 AA;
 Query Match 100.0%; Score 42; DB 9; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.62; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;
 QY 1 AMSTTDLEA 9
 Db 102 AMSTTDLEA 110
 RESULT 11
 AAY58473
 ID AAY58473 standard; protein; 154 AA.
 XX AC AAY58473;
 XX 10-APR-2000 (first entry)
 XX Hepatitis B virus (HBV) protein X.
 DE HBV protein X; proteasome activity; degradation; virus component;
 KW viral infection; inflammatory disease; anti-inflammatory; anti-HIV;
 KW virucide.
 XX OS Hepatitis b virus.
 XX PN WO9966065-A2.
 XX 23-DEC-1999.
 XX 10-JUN-1999; 99WO-GB01840.
 PR 13-JUN-1998; 98GB-0012756.
 PR 13-JUN-1998; 98GB-0012757.
 PR 13-JUN-1998; 98GB-0012758.
 PR 13-JUN-1998; 98GB-0012759.
 PR 13-JUN-1998; 98GB-0012760.
 XX (BRID-) BRIDGEHEAD TECHNOLOGIES LTD.
 PA Schmid HP, Petit F, Kloetzel PM, Jarrousse AS, Gautier K;
 PI Badaoui S, Mouzeyar S, Nicolas P;
 XX WPI; 2000-106109/09.
 DR Novel assay methods for identifying compounds which modulate and/or
 PT regulate proteasomal activity -
 XX Example 1; Page 8; 35pp; English.
 PS The invention relates to a novel assay for identifying compounds which
 CC inhibit viral replication and pathogenesis by increasing proteasomal
 CC degradation of viral components or molecules induced by viral infection.
 CC The method comprises reacting a compound with proteasomal protein (20S
 CC proteasomes separately with or without 19S and 11S complexes), viral
 CC gene product, and protein or peptide substrates; measuring protease
 CC activity; and identifying the compound as an inhibitor if the protease
 CC activity of the assay system is increased. The assays of the invention
 CC can be used to identify compounds which inhibit viral replication and
 CC pathogenesis, and modulate and/or regulate proteasome activity.
 CC Compounds which increase proteasomal degradation of viral components or
 CC molecules induced by viral infection are of value in the treatment of
 CC viral disease. Compounds which modulate proteasomal nuclease activity
 CC have use in the treatment of inflammatory disease, and AIDS in HIV

CC infected patients. The methods may also be used to generate resistance
 CC to bacterial or viral damage. Sequences AAY58472-Y8474 represent
 CC examples of viral proteins which affect proteasomal function.

XX SQ Sequence 154 AA;
 Query Match 100.0%; Score 42; DB 21; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.62;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 |||||
 DB 102 AMSTTDLEA 110

RESULT 12

AAV54047
 ID AAY54047 standard; Protein; 154 AA.

XX AC AAY54047;

XX DT 27-MAR-2000 (first entry)

XX DE Amino acid sequence of a HBV transactivating X protein.

XX KW HBV; HBV surface antigen-'S'-133 Oon strain (Met to Thr);
 DNA polymerase; large surface antigen; core protein;

XX KW transactivating X protein; hepatitis vaccine; HBV infection;
 hepatocellular carcinoma.

XX OS Hepatitis B virus.

XX PN WO9966048-A1.

XX PD 23-DEC-1999.

XX PF 19-JUN-1998; 98WO-SG00046.

XX PR 19-JUN-1998; 98WO-SG00046.

XX PA (GOVE-) GOVERNMENT REPUBLIC SINGAPORE.

XX PI Oon CJ, Lim GK, Zhao Y, Chen WN;

XX QY WPI; 2000-106104/09.

XX DR N-PSDB; AAZ37088.

XX PT New isolated hepatitis B virus strain, useful for, e.g. treatment of
 hepatitis infection

XX PS Disclosure; Page 42; 68pp; English.

XX CC The present sequence is encoded by the genome of an isolated strain of
 Hepatitis B virus designated human Hepatitis B virus (HBV) surface
 antigen-'S'-133 Oon strain (Met to Thr). The viral genome is deposited
 as ECCC accession numbers P97121501, P97121502 and P97121503. The
 nucleotide sequence was isolated from hepatocellular carcinoma (HCC).
 The nucleotide sequence encodes four overlapping proteins, which are
 a DNA polymerase, a large surface antigen, a core protein, and a
 transactivating X protein. The large surface antigen differs from the
 wild type sequence in that it contains a Thr at position 133 of the
 wild type sequence instead of a Met. The proteins are used to produce
 antibodies. The proteins, polynucleotide and antibodies can be used for
 detecting the novel HBV strain. The HBV polypeptides can also be used
 in hepatitis vaccines. The HBV novel strain polypeptides can be used
 to identify compounds for treating or preventing HBV infection or
 hepatocellular carcinoma.

XX SQ Sequence 154 AA;

Query Match 100.0%; Score 42; DB 21; Length 154;

Best Local Similarity 100.0%; Pred. No. 0.62;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 |||||
 DB 102 AMSTTDLEA 110

RESULT 13

AAV44351
 ID AAY44351 standard; Protein; 154 AA.

XX AC AAY44351;

XX DT 14-MAR-2000 (first entry)

XX DE Human hepatitis B virus trans-activating X protein sequence.

XX KW HBIG; Hepatitis B immunoglobulin; HBV; Hepatitis B virus;
 trans-activating X protein; mutant major surface antigen;

XX KW human hepatitis B viral genome; hepatocellular carcinoma; HBV infection;
 human hepatitis B virus surface antigen-'S'-145 Singapore strain;

XX OS Human hepatitis B virus.

XX PN WO9966047-A1.

XX PD 23-DEC-1999.

XX PF 19-JUN-1998; 98WO-SG00045.

XX PR 19-JUN-1998; 98WO-SG00045.

XX PA (GOVE-) GOVERNMENT REPUBLIC SINGAPORE.

XX PI Oon CJ, Lim GK, Leong AL, Zhao Y, Chen WN;

XX DR WPI; 2000-106103/09.

XX DR N-PSDB; AAZ29453.

XX PT New vaccine-escape mutant of hepatitis B virus and related proteins,
 nucleic acids and antibodies, useful for diagnosis, prevention and
 treatment

XX PS Disclosure; Fig 7; 65pp; English.

XX CC The present sequence is the trans-activating X protein deduced from the
 mutant human hepatitis B viral genome. This was isolated from a male,
 11 year old Singaporean child which had received standard HBIG and HB
 vaccine and was infected with the mutated strain designated human
 hepatitis B virus surface antigen-'S'-145 Singapore strain. A year
 later, this protein can be produced by recombinant technology and used in
 developing polyclonal or monoclonal antibodies and as a source of
 diagnostic oligonucleotides. The mutated major surface antigen is used to
 raise specific antibodies, to identify specific binding agents and, in
 CC vaccines or compositions for treatment or prevention of HBV infection and
 hepatocellular carcinoma. Antibodies are used in diagnosis or for
 screening donated body fluids or tissues.

XX SQ Sequence 154 AA;

Query Match 100.0%; Score 42; DB 21; Length 154;

Best Local Similarity 100.0%; Pred. No. 0.62;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 |||||
 DB 102 AMSTTDLEA 110

RESULT 14

ABJ07178
 ID ABJ07178 standard; Peptide; 8 AA.

XX

ABJ071178;
 14-NOV-2002 (first entry)
 Hepatitis B virus epitope #1396.
 Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 virucide; hepatotropic; antiinflammatory.
 Hepatitis B virus.
 WO200219986-A1.
 14-MAR-2002.
 08-SEP-2000; 2000WO-US24802.
 08-SEP-2000; 2000WO-US24802.
 (EPIM-) EPIMMUNE INC.
 (SETT/) SETTE A.
 Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 Celis E, Kubo RT, Grey HM, Chesnut RW;
 WPI; 2002-643192/69.
 Vaccine composition for treating or preventing hepatitis B virus (HBV)
 infection, and/or for stimulating an immune response to HBV, comprises
 a HBV peptide epitope -
 Disclosure; Page 137; 228pp; English.
 The present invention relates to a composition comprising at least one
 hepatitis B virus epitope. This can be used in the production of a
 vaccine for use in preventing or treating hepatitis B virus infection.
 The present sequence is a peptide described in the exemplification of the
 invention.
 Sequence 8 AA;
 Query Match 90.5%; Score 38; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 2 MSTTDLEA 9
 |||||
 1 MSTTDLEA 8
 SULT 15
 WO8117
 ABJ08117 standard; Peptide; 8 AA.
 ABJ08117;
 14-NOV-2002 (first entry)
 Hepatitis B virus epitope #2335.
 Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 virucide; hepatotropic; antiinflammatory.
 Hepatitis B virus.
 WO200219986-A1.
 14-MAR-2002.
 08-SEP-2000; 2000WO-US24802.
 08-SEP-2000; 2000WO-US24802.

PA (EPIM-) EPIMMUNE INC.
 PA (SETT/) SETTE A.
 PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 PI Celis E, Kubo RT, Grey HM, Chesnut RW;
 XX WPI; 2002-643192/69.
 DR Vaccine composition for treating or preventing hepatitis B virus (HBV)
 PT infection, and/or for stimulating an immune response to HBV, comprises
 PT a HBV peptide epitope -
 XX Disclosure; Page 160; 228pp; English.
 PS The present invention relates to a composition comprising at least one
 XX hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention.
 XX Sequence 8 AA;
 SQ Query Match 90.5%; Score 38; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MSTTDLEA 9
 |||||
 Db 1 MSTTDLEA 8
 Search completed: December 23, 2003, 08:44:01
 Job time : 26.8 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 25.8 Seconds
(without alignments)
55.370 Million cell updates/sec

Title: US-09-989-621-5
Perfect score: 41
Sequence: 1 EIRLKVFL 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A Genesec_19Jun03.*

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2: /SIDS1/gcgdata/genesec/genesecp-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/genesec/genesecp-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/genesec/genesecp-emb1/AA1983.DAT.*
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24: /SIDS1/gcgdata/genesec/genesecp-emb1/AA2003.DAT.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	9	14 AAR33297	Cytotoxic T-lympho
2	41	100.0	9	20 AAM52983	Hepatitis B virus
3	41	100.0	9	20 AAV24463	Hepatitis B virus
4	41	100.0	15	23 ABJ08326	Hepatitis B virus
5	41	100.0	15	23 ABJ08326	Hepatitis B virus
6	41	100.0	24	11 AAR07458	Peptide immunoreac
7	41	100.0	24	11 AAR07460	Peptide immunoreac
8	41	100.0	37	17 AAR94599	X-protein peptide.
9	41	100.0	154	6 AAP50461	Sequence of the an

10	41	100.0	154	9 AAP82174	Peptide encoded by
11	41	100.0	154	21 AAY58473	Hepatitis B virus
12	40	97.6	154	21 AAY44351	Human hepatitis B
13	37	90.2	154	21 AAY54047	Amino acid sequenc
14	36	87.8	424	22 AAY33217	Novel human secret
15	34	82.9	476	11 AAR07459	Peptide immunoreac
16	34	82.9	476	11 AAR07459	Helicobacter polyp
17	32	78.0	11	23 ABJ08203	Hepatitis B virus
18	32	78.0	11	23 ABJ08203	Hepatitis B virus
19	32	78.0	11	23 ABJ08203	Hepatitis B virus
20	32	78.0	11	23 ABJ08203	Hepatitis B virus
21	31	75.6	230	18 AAM32421	Novel human diagno
22	31	75.6	230	18 AAM32421	Mycobacterium tube
23	31	75.6	230	18 AAM32421	Mycobacterium tube
24	31	75.6	230	18 AAM32421	M. tuberculosis in
25	31	75.6	230	18 AAM32421	Mycobacterium tube
26	31	75.6	230	18 AAM32421	M. tuberculosis an
27	31	75.6	230	18 AAM32421	M. tuberculosis re
28	30	73.2	80	23 AAB71498	Drosophila melanog
29	30	73.2	80	23 AAB71498	Carp acyl coenzyme
30	30	73.2	80	23 AAB71498	Human polyprotein
31	30	73.2	110	22 AAG66775	Human ribosomal SI
32	30	73.2	126	22 AAM25829	Human protein sequ
33	29	70.7	39	22 AAM42193	Human polyprotein
34	29	70.7	60	22 AAM42193	Novel human enzyme
35	29	70.7	60	22 AAM42193	Novel human diagno
36	29	70.7	60	22 AAM42193	Human reproductive
37	29	70.7	60	22 AAM42193	Novel human diagno
38	29	70.7	134	16 AAR71563	Human secreted pro
39	29	70.7	164	22 AAG02409	Hepatitis B virus
40	29	70.7	216	20 AAY19974	Novel human diagno
41	29	70.7	228	16 AAR71113	B. burgdorferi ant
42	29	70.7	228	16 AAR71113	Mycobacterial prot
43	29	70.7	228	18 AAM18161	Mycobacterium tube
44	29	70.7	228	19 AAM63036	Mycobacterium tube
45	29	70.7	284	24 AAM50742	Mycobacterium tube
					Human secretory po

ALIGNMENTS

RESULT 1
AAR33297
ID AAR33297 standard; peptide; 9 AA.
AC AAR33297;
XX
DT 25-MAR-2003 (updated)
DT 02-JUL-1993 (first entry)
XX
DE Cytotoxic T-lymphocyte inducing peptide HBPoll126-134.
XX
KW MHC class I; major histocompatibility complex class I; CTL-response;
KW HBV; hepatitis B virus; vaccine; treatment; T-helper cell mediated.
XX
OS Synthetic.
XX
PN WO9303753-A1.
XX
PD 04-MAR-1993.
XX
PF 26-AUG-1992; 92WO-US07213.
XX
PR 26-AUG-1991; 91US-0749540.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Chisari FV, Ferrari C, Missale G, Penna A;
XX
DR WPI, 1993-093719/11.
XX
PT Cytotoxic T-lymphocyte-inducing peptide(s) from hepatitis B virus
PT - for preventing and treating virus infections, and identifying

PT individuals susceptible to developing chronic virus infection

PS Claim 18; Page 11; 76pp; English.

CC This peptide induces MHC class I restricted CTL responses against
 CC HBV (pref. restricted to HLA-A2, HLA31 or HLA-Aw68). It can be used
 CC for treating HBV infection, in vaccines against HBV, or may be
 CC joined to a second immunogenic peptide to elicit a T-helper cell
 CC mediated response.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 9 AA;

Query Match 100.0%; Score 41; DB 14; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

DB 1 EIRLKVFL 9

RESULT 2

AAW52983
 ID AAW52983 standard; peptide; 9 AA.

AC AAW52983;

DT 12-MAR-2002 (first entry)

DE Hepatitis B virus X protein peptide (residues 126-134).

KW HBV; X protein; cytotoxic T-lymphocyte; CTL; MHC class I;
 KW major histocompatibility complex; immunomodulator.

OS Hepatitis B virus.

PN KR98022440-A.

PD 06-JUL-1998.

PF 23-SEP-1996; 96KR-0041612.

PR 23-SEP-1996; 96KR-0041612.

PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.

PI Park SH, Chung MG, Lee HG, Yoon HS, Min SS, Lee TG, Lim JS;

PS WPI; 1999-300977/25.

PT Synthetic peptide having immunoregulating activities for hepatitis B
 PT virus -

PS Example 1; Page 4; 7pp; Korean.

CC The invention relates to peptides derived from the hepatitis B virus
 CC (HBV) X protein (AAW52970-AAW52973). The peptides are presented on major
 CC histocompatibility complex (MHC) class I molecules and act as cytotoxic
 CC T-lymphocyte (CTL) epitopes. Sequences AAW52974-AAW52984 represent HBV
 CC X protein-derived peptides used in an exemplification of the invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 41; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

DB 1 EIRLKVFL 9

RESULT 3

AAW24463
 ID AAW24463 standard; peptide; 9 AA.

AC AAW24463;

DT 23-SEP-1999 (first entry)

DE Hepatitis B virus X protein peptide #5.

KW Hepatitis B virus; HBV; X protein; cytotoxic T lymphocyte; liposome;
 KW CTL; antigen; immunity; liver cancer.

OS Hepatitis B virus.

OS Synthetic.

PN WO9336434-A1.

PD 22-JUL-1999.

PF 19-JAN-1998; 98WO-KR00010.

PR 19-JAN-1998; 98WO-KR00010.

PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.

PI Chang J, Cheong H, Cho S, Choi M, Hwang Y, Kim T;
 PI Lee K;

PS WPI; 1999-444387/37.

PT Hepatitis B virus protein X-derived peptide antigens used to
 PT stimulate cytotoxic T lymphocytes, useful for treatment of
 PT HBV-associated diseases, especially liver cancer

XX Claim 5; Page 24; 33pp; English.

CC The present invention describes peptide antigens AAW24459 to AAW24463
 CC derived from the X protein of hepatitis B virus (HBV) which are
 CC recognized by cytotoxic T lymphocytes (CTL). The peptide antigens
 CC derived from HBV X protein are useful for inducing CTLs against the
 CC virus or inducing immunological tolerance to the virus. pH-sensitive
 CC liposomes containing the peptide antigens are used to induce cellular
 CC immunity so that CTLs specific to the virus can be produced. This is
 CC useful for prevention and treatment of HBV-associated diseases,
 CC especially HBV-associated liver cancer. pH-sensitive liposomes permit
 CC the selective transportation of anti-cancer drugs.

XX Sequence 9 AA;

Query Match 100.0%; Score 41; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

DB 1 EIRLKVFL 9

RESULT 4

ABJ08926
 ID ABJ08926 standard; Peptide; 15 AA.

AC ABJ08926;

DT 14-NOV-2002 (first entry)

DE Hepatitis B virus epitope #3144.

KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 KW virucide; hepatotropic; antiinflammatory.

OS Hepatitis B virus.

CX WO200219986-A1.
 CX 14-MAR-2002.
 CX 08-SEP-2000; 2000WO-US24802.
 CX 08-SEP-2000; 2000WO-US24802.
 CX (EPIM-) EPIMUNE INC.
 CX (SETT/) SETTE A.
 CX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 CX Celis E, Kubo RT, Grey HM, Chesnut RW;
 CX WPI; 2002-643192/69.
 CX Vaccine composition for treating or preventing hepatitis B virus (HBV)
 CX infection, and/or for stimulating an immune response to HBV, comprises
 CX a HBV peptide epitope -
 CX Disclosure; Page 179; 228pp; English.
 CX The present invention relates to a composition comprising at least one
 CX hepatitis B virus epitope. This can be used in the production of a
 CX vaccine for use in preventing or treating hepatitis B virus infection.
 CX The present sequence is a peptide described in the exemplification of the
 CX invention.
 CX Sequence 15 AA;
 CX Query Match 100.0%; Score 41; DB 23; Length 15;
 CX Best Local Similarity 100.0%; Pred. No. 0.016;
 CX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CX
 CX 1 EIRLKVFL 9
 CX |||||
 CX 1 EIRLKVFL 9
 CX
 CX RESULT 5
 CX ABJ09218
 CX ID ABJ09218 standard; Peptide; 15 AA.
 CX AC ABJ09218;
 CX 14-NOV-2002 (first entry)
 CX Hepatitis B virus epitope #3436.
 CX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 CX virucide; hepatotropic; antiinflammatory.
 CX Hepatitis B virus.
 CX WO200219986-A1.
 CX 14-MAR-2002.
 CX 08-SEP-2000; 2000WO-US24802.
 CX 08-SEP-2000; 2000WO-US24802.
 CX (EPIM-) EPIMUNE INC.
 CX (SETT/) SETTE A.
 CX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 CX Celis E, Kubo RT, Grey HM, Chesnut RW;
 CX WPI; 2002-643192/69.
 CX Vaccine composition for treating or preventing hepatitis B virus (HBV)
 CX infection, and/or for stimulating an immune response to HBV, comprises

PT a HBV peptide epitope -
 XX Disclosure; Page 182; 228pp; English.
 XX The present invention relates to a composition comprising at least one
 XX hepatitis B virus epitope. This can be used in the production of a
 XX vaccine for use in preventing or treating hepatitis B virus infection.
 XX The present sequence is a peptide described in the exemplification of the
 XX invention.
 XX Sequence 15 AA;
 XX Query Match 100.0%; Score 41; DB 23; Length 15;
 XX Best Local Similarity 100.0%; Pred. No. 0.016;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 EIRLKVFL 9
 XX |||||
 XX 1 EIRLKVFL 9
 XX
 XX RESULT 6
 XX AAR07458
 XX ID AAR07458 standard; peptide; 24 AA.
 XX AC AAR07458;
 XX 25-MAR-2003 (updated)
 XX 04-FEB-1991 (first entry)
 XX Peptide immunoreactive with hepatitis B antibody (I).
 XX Hepatitis B antibody; diagnosis; hepatocellular carcinoma;
 XX immunoassay; chronic hepatitis.
 XX Synthetic.
 XX DB4011768-A.
 XX 18-OCT-1990.
 XX 11-APR-1990; 90DE-4011768.
 XX 14-APR-1989; 89JP-0095015.
 XX (OLYU) OLYMPUS OPTICAL CO LTD.
 XX Kumazawa T, Osanai M;
 XX WPI; 1990-321759/43.
 XX New polypeptide deriva. immune reactive with hepatitis B antibody
 XX - useful as immunoassay reagents, e.g. for diagnosing
 XX hepato:cellular carcinoma
 XX Claim 1; Page 8; 13pp; German.
 XX The peptide corresp. to a partic. fragment (amino acids 114-137) of
 XX the sequence encoded by the X-gene of HBV adr subtype. When
 XX immobilised on a carrier, e.g. BSA, latex, microtitre plate wells,
 XX etc., the peptides are useful as immunoassay reagents, for detecting
 XX Abs, esp. for diagnosis of hepatocellular carcinoma and chronic
 XX hepatitis. They can also be used as immunogens to raise antibodies.
 XX See also AAR07458-60.
 XX (Updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 24 AA;
 XX Query Match 100.0%; Score 41; DB 11; Length 24;
 XX Best Local Similarity 100.0%; Pred. No. 0.027;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 EIRLKVFL 9

Db 13 EIRLKVFL 21

RESULT 7

AA07460
ID AAR07460 standard; protein; 24 AA.

XX AC AAR07460;

XX DT 25-MAR-2003 (updated)

XX DT 04-FEB-1991 (first entry)

XX Key Peptide immunoreactive with hepatitis B antibody (III).

XX KW Hepatitis B antibody; diagnosis; hepatocellular carcinoma;

XX KW immunoassay; chronic hepatitis.

XX OS Synthetic.

XX PN DE4011768-A.

XX PD 18-OCT-1990.

XX PF 11-APR-1990; 90DE-4011768.

XX PR 14-APR-1989; 89JP-0095015.

XX PA (OLYU) OLYMPUS OPTICAL CO LTD.

XX PI Kumazawa T, Osanai M;

XX DR WPI; 1990-321759/43.

XX PT New polypeptide derivs. immune reactive with hepatitis B antibody

XX PT - useful as immunoassay reagents, e.g. for diagnosing

XX PT hepatocellular carcinoma

XX PS Claim 4; Page 8; 13pp; German.

XX CC The peptide corresp. to a partic. fragment (amino acids 114-137) of

XX CC the sequence encoded by the X-gene of HBV ayr subtype. When

XX CC immobilised on a carrier, e.g. BSA, latex, microtitre plate wells,

XX CC etc., the peptides are useful as immunoassay reagents, for detecting

XX CC Abc., esp. for diagnosis of hepatocellular carcinoma and chronic

XX CC hepatitis. They can also be used as immunogens to raise antibodies.

XX CC See also AAR07458-60.

XX CC (Updated on 25-MAR-2003 to correct PA field.)

XX CC Sequence 24 AA;

XX CC Query Match 100.0%; Score 41; DB 11; Length 24;

XX CC Best Local Similarity 100.0%; Pred. No. 0.027;

XX CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX CC QY 1 EIRLKVFL 9

XX CC Db 13 EIRLKVFL 21

XX CC RESULT 8

XX CC AAR94599

XX CC ID AAR94599 standard; Peptide; 37 AA.

XX CC AC AAR94599;

XX CC DT 13-JUL-1996 (first entry)

XX CC DE X-protein peptide.

XX CC X-protein; hepatitis B virus; Kunitz domain; transactivation;

XX CC site-directed mutagenesis; proteasome complex subunit; human;

XX CC XAPC7; S4; therapy; diagnostic; antigen; antibody; immunoassay;

XX CC KW

KW probe; primer.

XX Hepatitis B virus.

XX Key Location/Qualifiers

XX FT Misc-difference 10

XX FT /note= "Altered to Arg in mutant"

XX FT Misc-difference 22

XX FT /note= "Altered to Tyr in mutant"

XX FT Domain 22..35

XX FT /note= "Putative Kunitz domain"

XX FT Misc-difference 26

XX FT /note= "Altered to Val in mutant"

XX FT Misc-difference 27

XX FT /note= "Altered to Ser in mutant"

XX FT Misc-difference 28

XX FT /note= "Altered to Gln in mutant"

XX FT Misc-difference 29

XX FT /note= "Altered to Asp in mutant"

XX WO9611207-A1.

XX PN 18-APR-1996.

XX PD 05-OCT-1995; 95WO-US13426.

XX PF 06-OCT-1994; 94US-0319376.

XX PR (GEO) GEN HOSPITAL CORP.

XX PA Huang J, Liang TJ;

XX PI WPI; 1996-209804/21.

XX DR Prevention of interaction of HBV X and XAPC7 or S4 protein - using

XX PT a peptide which interferes with HBV infection, useful in treatment

XX PT of HBV infection

XX PS Claim 10; Fig 4; 45pp; English.

XX CC The sequence represents a fragment (amino acids 111-147) of hepatitis

XX CC B virus (HBV) X-protein (HBX), containing a putative Kunitz domain,

XX CC which is crucial for transactivation function of HBX. Key residues

XX CC in this domain have been mutated and transactivation properties of

XX CC mutants have been studied. HBX has been identified as interacting

XX CC with human proteasome complex subunits XAPC7 (C7, AAR94597) and S4

XX CC (AAR94600). Mutagenesis of critical residues has shown that this 2nd

XX CC domain is important for interaction with C7, and this phenotype

XX CC shows a close association with transactivation activity. Peptides

XX CC derived from the HBX protein may be used to interact with

XX CC proteasome subunits and interfere with HBV infection, and are thus

XX CC useful in therapy of hepatitis B. Such peptides are also useful as

XX CC antigens to generate polyclonal or monoclonal antibodies for

XX CC diagnostic applications. DNA probes and primers based on the

XX CC sequence may also be used to detect HBV infection.

XX CC Query Match 100.0%; Score 41; DB 17; Length 37;

XX CC Best Local Similarity 100.0%; Pred. No. 0.043;

XX CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX CC QY 1 EIRLKVFL 9

XX CC Db 16 EIRLKVFL 24

XX CC RESULT 9

XX CC AAP50461

XX CC ID AAP50461 standard; protein; 154 AA.

XX CC AC AAP50461;

XX CC KW

PR 13-JUN-1998; 98GB-0012759.
 PR 13-JUN-1998; 98GB-0012760.
 XX (BRID-) BRIDGEHEAD TECHNOLOGIES LTD.
 PA Schmid HP, Petit F, Kloetzel PM, Jarrousse AS, Gautier K;
 PI Badaoui S, Mouzeay S, Nicolas P;
 XX WPI; 2000-106109/09.
 DR PT Novel assay methods for identifying compounds which modulate and/or
 XX regulate proteasomal activity -
 XX Example 1; Page 8; 35pp; English.
 CC The invention relates to a novel assay for identifying compounds which
 CC inhibit viral replication and pathogenesis by increasing proteasomal
 CC degradation of viral components or molecules induced by viral infection.
 CC The method comprises reacting a compound with proteasomal protein (20S
 CC proteasomes separately with or without 19S and 11S complexes), viral
 CC gene product, and protein or peptide substrates; measuring protease
 CC activity; and identifying the compound as an inhibitor if the protease
 CC activity of the assay system is increased. The assays of the invention
 CC can be used to identify compounds which inhibit viral replication and
 CC pathogenesis, and modulate and/or regulate proteasome activity.
 CC Compounds which increase proteasomal degradation of viral components or
 CC molecules induced by viral infection are of value in the treatment of
 CC viral disease. Compounds which modulate proteasomal nuclease activity
 CC have use in the treatment of inflammatory disease, and AIDS in HIV
 CC infected patients. The methods may also be used to generate resistance
 CC to bacterial or viral damage. Sequences AAY58472-Y58474 represent
 CC examples of viral proteins which affect proteasomal function.
 XX SQ Sequence 154 AA;
 Query Match 100.0%; Score 41; DB 21; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRLKVFL 9
 DB 126 EIRLKVFL 134
 RESULT 12
 ID AAY44351
 AC AAY44351 standard; Protein; 154 AA.
 AC AAY44351;
 DT 14-MAR-2000 (first entry)
 DE Human hepatitis B virus trans-activating X protein sequence.
 XX HBIG; Hepatitis B immunoglobulin; HBV; Hepatitis B virus;
 KW trans-activating X protein; mutant major surface antigen;
 KW human hepatitis B viral genome; hepatocellular carcinoma; HBV infection;
 KW human hepatitis B virus surface antigen- 'S' - 145 Singapore strain;
 CS Human hepatitis B virus.
 OS
 XX WO9966047-A1.
 PN 23-DEC-1999.
 PD 19-JUN-1998; 98WO-SG00045.
 PF 19-JUN-1998; 98WO-SG00045.
 PR (GOVE-) GOVERNMENT REPUBLIC SINGAPORE.
 PA Oon CJ, Lim GK, Leong AL, Zhao Y, Chen WN;
 XX WPI; 2000-106104/09.
 DR N-PSDB; AAZ37088.
 DR PT New isolated hepatitis B virus strain, useful for, e.g. treatment of
 XX hepatitis infection -
 XX Disclosure; Page 42; 68pp; English.
 PS The present sequence is encoded by the genome of an isolated strain of
 CC Hepatitis B virus designated human Hepatitis B virus (HBV) surface

XX WPI; 2000-106103/09.
 DR N-PSDB; AAZ29453.
 XX New vaccine-escape mutant of hepatitis B virus and related proteins,
 PT nucleic acids and antibodies, useful for diagnosis, prevention and
 PT treatment -
 XX Disclosure; Fig 7; 65pp; English.
 XX The present sequence is the trans-activating X protein deduced from the
 CC mutant human hepatitis B viral genome. This was isolated from a male,
 CC 11 year old Singaporean child which had received standard HBIG and HB
 CC vaccine and was infected with the mutated strain designated human
 CC hepatitis B virus surface antigen- 'S' - 145 Singapore strain a year
 CC later. This protein can be produced by recombinant technology and used in
 CC developing polyclonal or monoclonal antibodies and as a source of
 CC diagnostic oligonucleotides. The mutated major surface antigen is used to
 CC raise specific antibodies, to identify specific binding agents and, in
 CC vaccines or compositions for treatment or prevention of HBV infection and
 CC hepatocellular carcinoma. Antibodies are used in diagnosis or for
 CC screening donated body fluids or tissues.
 XX SQ Sequence 154 AA;
 Query Match 97.6%; Score 40; DB 21; Length 154;
 Best Local Similarity 88.9%; Pred. No. 0.35;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRLKVFL 9
 DB 126 EVRLKVFL 134
 RESULT 13
 ID AAY54047
 AC AAY54047 standard; Protein; 154 AA.
 AC AAY54047;
 DT 27-MAR-2000 (first entry)
 DE Amino acid sequence of a HBV transactivating X protein.
 XX HBV; HBV surface antigen- 'S' - 133 Oon strain (Met to Thr);
 KW DNA polymerase; large surface antigen; core protein;
 KW transactivating X protein; hepatitis vaccine; HBV infection;
 KW hepatocellular carcinoma.
 XX Hepatitis B virus.
 OS
 XX WO9966048-A1.
 PN 23-DEC-1999.
 PD 19-JUN-1998; 98WO-SG00046.
 PF 19-JUN-1998; 98WO-SG00046.
 PR (GOVE-) GOVERNMENT REPUBLIC SINGAPORE.
 PA Oon CJ, Lim GK, Zhao Y, Chen WN;
 XX WPI; 2000-106104/09.
 DR N-PSDB; AAZ37088.
 DR PT New isolated hepatitis B virus strain, useful for, e.g. treatment of
 XX hepatitis infection -
 XX Disclosure; Page 42; 68pp; English.
 PS The present sequence is encoded by the genome of an isolated strain of
 CC Hepatitis B virus designated human Hepatitis B virus (HBV) surface

CC antigen-'S'-133 Con strain (Vet to Thr). The viral genome is deposited
 CC as ECCC accession numbers P97121501, P97121502 and P97121503. The
 CC nucleotide sequence was isolated from hepatocellular carcinoma (HCC).
 CC The nucleotide sequence encodes four overlapping proteins, which are
 CC a DNA polymerase, a large surface antigen, a core protein, and a
 CC transactivating X protein. The large surface antigen differs from the
 CC wild type sequence in that it contains a Thr at position 133 of the
 CC wild type sequence instead of a Met. The proteins are used to produce
 CC antibodies. The proteins, polynucleotide and antibodies can be used for
 CC detecting the novel HBV strain. The HBV polypeptides can also be used
 CC in hepatitis vaccines. The HBV novel strain polypeptides can be used
 CC to identify compounds for treating or preventing HBV infection or
 CC hepatocellular carcinoma.

CC Sequence 154 AA;
 CC Query Match 90.2%; Score 37; DB 21; Length 154;
 CC Best Local Similarity 77.8%; Pred. No. 1.7;
 CC Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CC 1 EIRLKVFL 9
 CC 126 EIRLKIYVL 134

CC RESULT 14
 CC AU33217
 CC D AAU33217 standard; Protein; 424 AA.

CC AAU33217;

CC 18-DEC-2001 (first entry)

CC Novel human secreted protein #3708.

CC Human; vaccination; gene therapy; nutritional supplement;
 CC stem cell proliferation; hematopoiesis; nerve tissue regeneration;
 CC immune suppression; immune stimulation; anti-inflammatory; leukaemia.

CC Homo sapiens.

CC WO200179449-A2.

CC 25-OCT-2001.

CC 16-APR-2001; 2001WO-US08656.

CC 18-APR-2000; 2000US-0552929.

CC 26-JAN-2001; 2001US-0770160.

CC (HYSE-) HYSEQ INC.

CC Tang YT, Liu C, Drmanac RT;

CC WPI; 2001-611725/70.

CC Nucleic acids encoding a range of human polypeptides, useful in genetic
 CC vaccination, testing and therapy -

CC Claim 20; Page 733; 765pp; English.

CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to

CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU33217-134 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.

CC Sequence 424 AA;

CC Query Match 87.8%; Score 36; DB 22; Length 424;
 CC Best Local Similarity 87.5%; Pred. No. 8.6;
 CC Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CC 1 EIRLKVFL 8
 CC 250 EVRLKVFL 257

CC RESULT 15

CC AAR07459

CC ID AAR07459 standard; protein; 24 AA.

CC AAR07459;

CC 25-MAR-2003 (updated)

CC 04-FEB-1991 (first entry)

CC Peptide immunoreactive with hepatitis B antibody (II).

CC Hepatitis B antibody; diagnosis; hepatocellular carcinoma;

CC immunocassay; chronic hepatitis.

CC Synthetic.

CC DB4011768-A.

CC 18-OCT-1990.

CC 11-APR-1990; 90DB-4011768.

CC 14-APR-1989; 89JP-0095015.

CC (OLYU) OLYMPUS OPTICAL CO LTD.

CC Kumazawa T, Osanai M;

CC WPI; 1990-321759/43.

CC New polypeptide derivs. immune reactive with hepatitis B antibody

CC - useful as immunocassay reagents, e.g. for diagnosing

CC hepatocellular carcinoma

CC Claim 3; Page 8; 13pp; German.

CC The peptide corresp. to a partic. fragment (amino acids 114-137) of

CC the sequence encoded by the X-gene of HBV adw subtype. When

CC immobilised on a carrier, e.g. BSA, latex, microtitre plate wells,

CC etc., the peptides are useful as immunocassay reagents, for detecting

CC Abs. esp. for diagnosis of hepatocellular carcinoma and chronic

CC hepatitis. They can also be used as immunogens to raise antibodies.

CC See also AAR07458-60.

CC (Updated on 25-MAR-2003 to correct PA field.)

CC Sequence 24 AA;

CC Query Match 82.9%; Score 34; DB 11; Length 24;

CC Best Local Similarity 77.8%; Pred. No. 1;

CC Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CC 1 EIRLKVFL 9
 CC 13 EIRLMIFVL 21

Search completed: December 23, 2003, 08:44:04
Job time : 26.8 secs

GenCore version 5.1.6
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M protein - protein search, using sw model

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(without alignments)
55.370 Million cell updates/sec

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total number of hits satisfying chosen parameters: 1107863

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	9	15	Peptide fragment (
2	55	100.0	9	20	Hepatitis B virus
3	55	100.0	9	20	Hepatitis B virus
4	55	100.0	18	9	Antigenic determin
5	55	100.0	24	11	Peptide immunoreac
6	55	100.0	37	17	X-protein peptide.
7	55	100.0	134	16	Hepatitis B virus
8	55	100.0	154	6	Sequence of the an
9	55	100.0	154	9	Peptide encoded by

10	52	94.5	24	11	AA07458	Peptide immunoreac
11	52	94.5	24	11	AA07459	Peptide immunoreac
12	52	94.5	154	21	AA58473	Hepatitis B virus
13	52	94.5	154	21	AA54047	Amino acid sequenc
14	46	83.6	9	23	AB709615	Hepatitis B virus
15	45	83.6	16	6	AA50459	Sequence of an ant
16	43	78.2	154	21	AA44351	Hepatitis B virus
17	43	78.2	1146	22	AAU35618	Human hepatitis B
18	42	76.4	32	22	AA04714	Haemophilus influe
19	42	76.4	146	22	AA66920	Hepatitis B virus
20	42	76.4	153	22	AA04712	HBV HBx protein.
21	41	74.5	484	22	AB59287	Hepatitis B virus
22	41	74.5	614	22	AA72004	Drosophila melanog
23	40	72.7	462	23	ABP38872	Chondrus crispus s
24	38	69.1	395	24	ABR41447	Staphylococcus epi
25	38	69.1	766	22	ABG13668	Human DITP zinc f
26	38	69.1	873	22	ABG04685	Novel human diagno
27	37	67.3	19	22	ABG23526	Novel human diagno
28	37	67.3	73	22	AA09408	Human immune/haema
29	37	67.3	92	21	AA55534	Arabidopsis thalia
30	37	67.3	246	23	ABP26242	Streptococcus poly
31	37	67.3	338	24	ABP0927	N. gonorrhoeae ami
32	37	67.3	715	22	AA96249	Putative P. abyssi
33	37	67.3	936	15	AA52579	Recombinant collag
34	37	67.3	1008	19	AA63721	C. histolyticum CH
35	37	67.3	1118	22	AA65579	Human cancer-relat
36	36	65.5	9	24	ABR01894	Human cancer-relat
37	36	65.5	9	24	ABR02082	Human cancer-relat
38	36	65.5	9	24	ABR02113	Human cancer-relat
39	36	65.5	9	24	ABR02351	Human cancer-relat
40	36	65.5	9	24	ABR02553	Human cancer-relat
41	36	65.5	9	24	ABR02736	Human cancer-relat
42	36	65.5	9	24	ABR02744	Human cancer-relat
43	36	65.5	9	24	ABR02938	Human cancer-relat
44	36	65.5	9	24	ABR02951	Human cancer-relat
45	36	65.5	9	24	ABR03148	Human cancer-relat

ALIGNMENTS

RESULT 1

AA059183

ID AA059183 standard; peptide; 9 AA.

XX AA059183;

AC

XX

DT 25-MAR-2003 (updated)

DT 03-MAY-1995 (first entry)

XX

DE Peptide fragment (1.0216) of HBV binds HLA-A2.1.

XX

KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;

KW HIV; core antigen; surface antigen; pharmaceutical composition;

KW in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule;

KW major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor;

XX human leukocyte antigen.

OS Hepatitis B Virus adr.

XX

PN WO9420127-A1.

XX

PD 15-SEP-1994.

XX

PF 04-MAR-1994; 94WO-US02353.

XX

PR 05-MAR-1993; 93US-0027146.

PR

PR 04-JUN-1993; 93US-0073205.

PR

PR 29-NOV-1993; 93US-0159184.

XX

PA (CYTE-) CYTEL CORP.

XX

PI Grey HM, Kast WM, Sette A, Sidney J;

25-MAR-2003 (updated)
 06-JAN-1991 (first entry)
 Antigenic determinant of HBxAg.
 Antigenic peptide; HBxAg; antigenic polymer; assay; diagnosis;
 Hepatitis B virus.
 WO8809340-A.
 01-DEC-1988.
 24-MAY-1988; 85WO-US01719.
 26-MAY-1987; 87US-0054424.
 (SCHI) SCRIPPS CLINIC & RES FOUND.
 Moriarty AM;
 WPI; 1988-353925/49.
 Antigenic synthetic polypeptide(s) - contg. an amino acid sequence
 corresponding to an antigenic determinant of hepatitis B virus, HBxAg
 Claim 4; Page 90; 106pp; English.
 The peptide and antibodies reactive with it are used in diagnostic
 assays for HBxAg in a body sample. They can also be used in affinity
 matrices for isolation and purification.
 (Updated on 25-MAR-2003 to correct PA field.)
 Sequence 18 AA;
 Query Match 100.0%; Score 55; DB 9; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CLFKDWHEEL 9
 |||||
 1 CLFKDWHEEL 9

SULT 5
 207460
 AAR07460 standard; protein; 24 AA.
 AAR07460;
 25-MAR-2003 (updated)
 04-FEB-1991 (first entry)
 Peptide immunoreactive with hepatitis B antibody (III).
 Hepatitis B antibody; diagnosis; hepatocellular carcinoma;
 immunoassay; chronic hepatitis.
 Synthetic.
 DE4011768-A.
 18-OCT-1990.
 11-APR-1990; 90DE-4011768.
 14-APR-1989; 89JP-0095015.
 (OLYU) OLYMPUS OPTICAL CO LTD.
 Kumazawa T, Oeanai M;
 WPI; 1990-321759/43.

XX New polypeptide derivs. immune reactive with hepatitis B antibody
 PT - useful as immunoassay reagents, e.g. for diagnosing
 PT hepato:cellular carcinoma
 XX
 PS Claim 4; Page 8; 13pp; German.
 XX
 CC The peptide corresp. to a partic. fragment (amino acids 114-137) of
 CC the sequence encoded by the X-gene of HBV avr subtype. When
 CC immobilised on a carrier, e.g. BSA, latex, microtitre plate wells,
 CC etc., the peptides are useful as immunoassay reagents for detecting
 CC Abs, esp. for diagnosis of hepatocellular carcinoma and chronic
 CC hepatitis. They can also be used as immunogens to raise antibodies.
 CC See also AAR07458-60.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 24 AA;
 Query Match 100.0%; Score 55; DB 11; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.038;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CLFKDWHEEL 9
 |||||
 DB 2 CLFKDWHEEL 10

RESULT 6
 AAR94599
 ID AAR94599 standard; Peptide; 37 AA.
 XX
 AC AAR94599;
 XX
 DT 13-JUL-1996 (first entry)
 XX
 DE X-protein peptide.
 KW X-protein; hepatitis B virus; Kunitz domain; transactivation;
 KW site-directed mutagenesis; proteasome complex subunit; human;
 KW XAPC7; S4; therapy; diagnostic; antigen; antibody; immunoassay;
 KW probe; primer.
 XX
 OS Hepatitis B virus.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 10 /note= "Altered to Arg in mutant"
 FT Misc-difference 22 /note= "Altered to Tyr in mutant"
 FT Domain 22..35 /note= "Putative Kunitz domain"
 FT Misc-difference 26 /note= "Altered to Val in mutant"
 FT Misc-difference 27 /note= "Altered to Ser in mutant"
 FT Misc-difference 28 /note= "Altered to Gln in mutant"
 FT Misc-difference 29 /note= "Altered to Asp in mutant"
 XX
 PN WO9611207-A1.
 XX
 PD 18-APR-1996.
 XX
 PF 05-OCT-1995; 95WO-US13426.
 XX
 PR 06-OCT-1994; 94US-0319376.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Huang J, Liang TJ;
 XX
 DR WPI; 1996-209804/21.

Sequence	154 AA;
----------	---------

Query Match 100.0%; Score 55; DB 6; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CLFKDWEEL 9
 |||||
 115 CLFKDWEEL 123

SULT 9
 82174

AAP82174 standard; protein; 154 AA.

AAP82174;

25-MAR-2003 (updated)
 01-JAN-1980 (first entry)

Peptide encoded by HBxAg gene.

Antigenic peptide; HBxAg; antigenic polymer; assay; diagnosis;

Hepatitis B virus.

Key Location/Qualifiers
 Region 23..0
 /label=Portion of HBxAg expressed by SVBHV-3
 Region 100..115
 /label=Synthetic polypeptide 99
 Region 115..131
 /label=Synthetic polypeptide 100
 Region 144..154
 /label=Synthetic polypeptide 142

W08809340-A.

01-DEC-1988.

24-MAY-1988; 88WO-US01719.

26-MAY-1987; 87US-0054424.

(SCRI) SCRIPPS CLINIC & RES FOUND.

Moriarty AM;

WPI; 1988-353925/49.

Antigenic synthetic polypeptide(s) - contg. an amino acid sequence
 corresponding to an antigenic determinant of hepatitis B virus, HBxAg

Disclosure; Fig. 6; 106pp; English.

The polypeptide is encoded by the HBxAg gene.
 (Updated on 25-MAR-2003 to correct PA field.)

Sequence 154 AA;

Query Match 100.0%; Score 55; DB 9; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CLFKDWEEL 9
 |||||
 115 CLFKDWEEL 123

SULT 10
 07458

AAR07458 standard; peptide; 24 AA.

AAR07458;

XX 25-MAR-2003 (updated)
 DT 04-FEB-1991 (first entry)
 XX Peptide immunoreactive with hepatitis B antibody (I).
 XX Hepatitis B antibody; diagnosis; hepatocellular carcinoma;
 KW immunoassay; chronic hepatitis.
 XX Synthetic.
 XX DE4011768-A.
 XX 18-OCT-1990.
 XX 11-APR-1990; 90DE-4011768.
 XX 14-APR-1989; 89JP-0095015.
 XX (OLYU) OLYMPUS OPTICAL CO LTD.
 XX Kumazawa T, Osanai M;
 XX WPI; 1990-321759/43.
 XX New polypeptide derivs. immune reactive with hepatitis B antibody
 PT - useful as immunoassay reagents, e.g. for diagnosing
 PT hepato:cellular carcinoma
 XX Claim 1; Page 8; 13pp; German.
 XX The peptide corresp. to a partic. fragment (amino acids 114-137) of
 CC the sequence encoded by the X-gene of HBV adr subtype. When
 CC immobilised on a carrier, e.g. BSA, latex, microtitre plate wells,
 CC etc., the peptides are useful as immunoassay reagents, for detecting
 CC Abs, esp. for diagnosis of hepatocellular carcinoma and chronic
 CC hepatitis. They can also be used as immunogens to raise antibodies.
 CC See also AAR07458-60.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 24 AA;

Query Match 94.5%; Score 52; DB 11; Length 24;
 Best Local Similarity 88.9%; Pred. No. 0.11;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CLFKDWEEL 9
 |||||
 Db 2 CVFKDWEEL 10

RESULT 11

AAR07459
 ID AAR07459 standard; protein; 24 AA.

XX AAR07459;

XX 25-MAR-2003 (updated)

DT 04-FEB-1991 (first entry)

XX Peptide immunoreactive with hepatitis B antibody (II).

XX Hepatitis B antibody; diagnosis; hepatocellular carcinoma;
 KW immunoassay; chronic hepatitis.

XX Synthetic.

XX DE4011768-A.

XX 18-OCT-1990.

XX 11-APR-1990; 90DE-4011768.

14-APR-1989; 89JP-0095015.
 (OLYU) OLYMPUS OPTICAL CO LTD.
 Kumazawa T, Osanai M;
 WPI; 1990-321759/43.
 New polypeptide derivs. immune reactive with hepatitis B antibody
 - useful as immunoassay reagents, e.g. for diagnosing
 hepato:cellular carcinoma
 Claim 3; Page 8; 13pp; German.
 The peptide corresp. to a partic. fragment (amino acids 114-137) of
 the sequence encoded by the X-gene of HBV adw subtype. When
 immobilised on a carrier, e.g. BSA, latex, microtitre plate wells,
 etc., the peptides are useful as immunoassay reagents, for detecting
 Abs, esp. for diagnosis of hepatocellular carcinoma and chronic
 hepatitis. They can also be used as immunogens to raise antibodies.
 See also AR07458-60.
 (Updated on 25-MAR-2003 to correct PA field.)
 Sequence 24 AA;
 Query Match 94.5%; Score 52; DB 11; Length 24;
 Best Local Similarity 88.9%; Pred. No. 0.11;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 1 CLFKDWEEL 9
 :|||||
 2 CVFKDWEEL 10

RESULT 12
 AY58473
 AY58473 standard; protein; 154 AA.
 AY58473;
 10-APR-2000 (first entry)
 Hepatitis B virus (HBV) protein X.
 HBV protein X; proteasome activity; degradation; virus component;
 viral infection; inflammatory disease; anti-inflammatory; anti-HIV;
 virucide.
 Hepatitis b virus.
 WO9966065-A2.
 23-DEC-1999.
 10-JUN-1999; 99WO-GB01840.
 13-JUN-1998; 98GB-0012756.
 13-JUN-1998; 98GB-0012757.
 13-JUN-1998; 98GB-0012758.
 13-JUN-1998; 98GB-0012759.
 13-JUN-1998; 98GB-0012760.
 (BRID-) BRIDGEHEAD TECHNOLOGIES LTD.
 Schmid HP, Petit F, Kloetzel PM, Jarrousse AS, Gautier K;
 Badaoui S, Mouzeyar S, Nicolas P;
 WPI; 2000-106109/09.
 Novel assay methods for identifying compounds which modulate and/or
 regulate proteasomal activity -
 Example 1; Page 8; 35pp; English.

XX The invention relates to a novel assay for identifying compounds which
 CC inhibit viral replication and pathogenesis by increasing proteasomal
 CC degradation of viral components or molecules induced by viral infection.
 CC The method comprises reacting a compound with proteasomal protein (20S
 CC proteasomes separately with or without 19S and 11S complexes), viral
 CC gene product, and protein or peptide substrates; measuring protease
 CC activity; and identifying the compound as an inhibitor if the protease
 CC activity of the assay system is increased. The assays of the invention
 CC can be used to identify compounds which inhibit viral replication and
 CC pathogenesis, and modulate and/or regulate proteasome activity.
 CC Compounds which increase proteasomal degradation of viral components or
 CC molecules induced by viral infection are of value in the treatment of
 CC viral disease. Compounds which modulate proteasomal nuclease activity
 CC have use in the treatment of inflammatory disease, and AIDS in HIV
 CC infected patients. The methods may also be used to generate resistance
 CC to bacterial or viral damage. Sequences AAY58472-Y58474 represent
 CC examples of viral proteins which affect proteasomal function.
 XX
 SQ Sequence 154 AA;
 Query Match 94.5%; Score 52; DB 21; Length 154;
 Best Local Similarity 88.9%; Pred. No. 0.75;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CLFKDWEEL 9
 :|||||
 DB 115 CVFKDWEEL 123

RESULT 13
 AAY54047
 ID AAY54047 standard; Protein; 154 AA.
 XX AAY54047;
 AC AAY54047;
 XX 27-MAR-2000 (first entry)
 DT Amino acid sequence of a HBV transactivating X protein.
 XX
 DE HBV; HBV surface antigen-'S'-133 Oon strain (Met to Thr);
 KW DNA polymerase; large surface antigen; core protein;
 KW transactivating X protein; hepatitis vaccine; HBV infection;
 KW hepatocellular carcinoma.
 XX
 OS Hepatitis B virus.
 XX
 PN WO9966048-A1.
 XX
 PD 23-DEC-1999.
 XX
 PF 19-JUN-1998; 98WO-SG000046.
 XX
 PR 19-JUN-1998; 98WO-SG000046.
 XX
 PA (GOVE-) GOVERNMENT REPUBLIC SINGAPORE.
 XX
 PI Oon CJ, Lim GK, Zhao Y, Chen WN;
 PI
 DR WPI; 2000-106104/09.
 DR N-PSDB; AAZ37088.
 XX
 PT New isolated hepatitis B virus strain, useful for, e.g. treatment of
 PT hepatitis infection -
 XX
 PS Disclosure; Page 42; 68pp; English.
 XX
 CC The present sequence is encoded by the genome of an isolated strain of
 CC Hepatitis B virus designated human Hepatitis B virus (HBV) surface
 CC antigen-'S'-133 Oon strain (Met to Thr). The viral genome is deposited
 CC as ECCC accession numbers P97121501, P97121502 and P97121503. The
 CC nucleotide sequence was isolated from hepatocellular carcinoma (HCC).
 CC The nucleotide sequence encodes four overlapping proteins, which are

a DNA polymerase, a large surface antigen, a core protein, and a transactivating X protein. The large surface antigen differs from the wild type sequence in that it contains a Thr at position 133 of the wild type sequence instead of a Met. The proteins are used to produce antibodies. The proteins, polynucleotide and antibodies can be used for detecting the novel HBV strain. The HBV polypeptides can also be used in hepatitis vaccines. The HBV novel strain polypeptides can be used to identify compounds for treating or preventing HBV infection or hepatocellular carcinoma.

Sequence 154 AA;

Query Match 94.5%; Score 52; DB 21; Length 154;
Best Local Similarity 88.9%; Pred. No. 0.75; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 CLFKDWEEL 9

|||||

115 CVFKDWEEL 123

SULT 14
J09615

ABJ09615 standard; Peptide; 9 AA.

ABJ09615;

14-NOV-2002 (first entry)

Hepatitis B virus analogue #227.

Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis; virucide; hepatotropic; antiinflammatory.

Hepatitis B virus.

WO200219986-A1.

14-MAR-2002.

08-SEP-2000; 2000WO-US24802.

08-SEP-2000; 2000WO-US24802.

(EPIM-) EPIMUNE INC.

(SETT/) SETTE A.

Sette A, Sidney J, Southwood S, Vitello MA, Livingstone BD;
Cellis E, Kubo RT, Grey HM, Cheenut RW;

WPI; 2002-643192/69.

Vaccine composition for treating or preventing hepatitis B virus (HBV) infection, and/or for stimulating an immune response to HBV, comprises a HBV peptide epitope -

Disclosure; Page 193; 228pp; English.

The present invention relates to a composition comprising at least one hepatitis B virus epitope. This can be used in the production of a vaccine for use in preventing or treating hepatitis B virus infection. The present sequence is a peptide described in the exemplification of the invention.

Sequence 9 AA;

Query Match 83.6%; Score 46; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 LFKDWEEL 9

|||||

2 LFKDWEEL 9

RESULT 15

AAP50459

ID AAP50459 standard; Protein; 16 AA.

XX AAP50459;

AC AAP50459;

DT 25-MAR-2003 (updated)

DT 27-SEP-1991 (first entry)

XX

XX

DE

DE

XX

XX

OS

XX

XX

PN

WO8503950-A.

PD

12-SEP-1985.

XX

XX

PF

06-MAR-1985; 85WO-US00359.

XX

XX

PR

07-SEP-1984; 84US-0648142.

PR

08-MAR-1984; 84US-0587570.

PR

26-MAY-1987; 87US-0054424.

XX

XX

PA

(SCRI) SCRIPPS CLINIC & RES FOUND.

XX

XX

PI

Moriarty AM, Alexander H, Lerner RA;

XX

XX

DR

WFI; 1985-236420/38.

XX

XX

PT

Expression vector contg. Gene coding for hepatitis B HBxAg -

PT

useful in diagnostic systems for detection of HBxAg and its

PT

antibody in body samples

XX

XX

PS

Claim 10ii; Page 83; 86pp; English.

XX

XX

CC

The inventors claim an antigenic synthetic polypeptide containing

CC

about 6 to about 40 AA residues corresponding in AA residue sequence

CC

to an antigenic determinant of HBxAg (see AAP50458-P50460). The

CC

antigenic polypeptides may be used in a diagnostic assay system for

CC

determining the presence of HBxAg in a body sample.

CC

(Updated on 25-MAR-2003 to correct PF field.)

CC

(Updated on 25-MAR-2003 to correct PA field.)

XX

SQ Sequence 16 AA;

Query Match 83.6%; Score 46; DB 6; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.7; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LFKDWEEL 9

|||||

Db 1 LFKDWEEL 8

Search completed: December 23, 2003, 08:44:03
Job time : 27.8 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

1 protein - protein search, using sw model

on on: December 23, 2003, 08:39:57 ; Search time 25.8 Seconds
(without alignments)
55.370 Million cell updates/sec

file: US-09-989-621-2

effect score: 45

quence: 1 VLHKRTLGL 9

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 1107863 seqs, 158726573 residues

tal number of hits satisfying chosen parameters: 1107863

nimum DB seq length: 0

ximum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

tabase :

```

1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
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21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	45	100.0	9 15 AAR59193	Peptide fragment (
2	45	100.0	9 20 AAR52980	Hepatitis B virus
3	45	100.0	9 20 AA124460	Hepatitis B virus
4	45	100.0	9 23 ABJ06345	Hepatitis B virus
5	45	100.0	9 23 ABJ06875	Hepatitis B virus
6	45	100.0	9 23 ABJ07613	Hepatitis B virus
7	45	100.0	9 23 ABJ08841	Hepatitis B virus
8	45	100.0	9 23 ABJ09133	Hepatitis B virus
9	45	100.0	10 20 AAR52970	Hepatitis B virus

10	45	100.0	10 23 ABJ06135	Hepatitis B virus
11	45	100.0	10 23 ABJ06665	Hepatitis B virus
12	45	100.0	10 23 ABJ07674	Hepatitis B virus
13	45	100.0	11 23 ABJ07128	Hepatitis B virus
14	45	100.0	15 23 ABJ08988	Hepatitis B virus
15	45	100.0	15 23 ABJ09280	Hepatitis B virus
16	45	100.0	134 16 AAR71563	Sequence of the an
17	45	100.0	154 6 AAP50461	Peptide encoded by
18	45	100.0	154 9 AAP82174	Hepatitis B virus
19	45	100.0	154 21 AAY58473	Hepatitis B virus
20	45	100.0	154 21 AAY44351	Human hepatitis B
21	42	93.3	9 15 AAR59182	Peptide fragment (
22	42	93.3	10 15 AAR61555	Peptide fragment (
23	41	91.1	8 23 AARJ07034	Hepatitis B virus
24	41	91.1	22 9 AAP82173	Antigenic determin
25	39	86.7	154 21 AAY54047	Amino acid sequenc
26	37	82.2	324 23 ABP40151	Staphylococcus epi
27	36	80.0	505 22 AB958791	Drosophila melanog
28	35	77.8	8 23 ABJ06134	Hepatitis B virus
29	35	77.8	8 23 ABJ06664	Hepatitis B virus
30	35	77.8	8 23 ABJ07426	Hepatitis B virus
31	35	77.8	9 23 ABJ07065	Hepatitis B virus
32	35	77.8	10 23 ABJ06965	Hepatitis B virus
33	35	77.8	10 23 ABJ07687	Hepatitis B virus
34	35	77.8	144 22 AB958535	Drosophila melanog
35	35	77.8	165 22 AB958534	Drosophila melanog
36	35	77.8	452 22 AAG70913	S cerevisiae apopt
37	33	73.3	102 21 AAB40688	Human ORFX ORF452
38	33	73.3	143 23 AB993600	Herbicidally activ
39	33	73.3	215 23 AB993441	Herbicidally activ
40	33	73.3	630 23 AB10103	Mouse immediate ea
41	33	73.3	1869 22 AB958651	Drosophila melanog
42	32	71.1	23 21 AB28310	Human secreted pep
43	32	71.1	53 22 AAJ39919	Propionibacterium
44	32	71.1	90 23 ABP04610	Human ORFX protein
45	32	71.1	263 21 AAG30271	Arabidopsis thalia

ALIGNMENTS

RESULT 1

AAR59193
ID AAR59193 standard; peptide; 9 AA.

XX AAR59193;

XX 25-MAR-2003 (updated)

DT 03-MAY-1995 (first entry)

XX Peptide fragment (1.0391) of HBV binds HLA-A2.1.

DE antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;
KW HIV1; core antigen; surface antigen; pharmaceutical composition;
KW in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule;
KW major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor;
KW human leukocyte antigen.

XX Hepatitis B Virus adw.

XX WO9420127-A1.

XX 15-SEP-1994.

XX 04-MAR-1994; 94WO-US02353.

XX 05-MAR-1993; 93US-0027146.

PR 04-JUN-1993; 93US-0073205.

PR 29-NOV-1993; 93US-0159184.

XX (CYTE-) CYTEL CORP.

PI Grey HM, Kast WM, Sette A, Sidney J;

CX WPI; 1994-302678/37.
 CX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
 CX for treatment or prophylaxis of cancer, virus infection or
 CX autoimmune diseases.
 CX
 CX Example 5; Page 103; 138pp; English.
 CX
 CX AAR59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1
 CX binding motif. These peptides bind HLA-A2.1 and have a binding affinity
 CX of at least 1% as compared to a reference peptide (AAR71293). AAR59193
 CX has an IC50 of 0.0007 and the sequence occurs at position 1539 in the HBV
 CX "X" protein (as given in the specification). The peptides of the
 CX invention can induce cytotoxic T lymphocytes which can react with target
 CX cells. They can be used for the treatment or prophylaxis of cancer, eg.
 CX prostate cancer or lymphoma, etc.
 CX (Updated on 25-MAR-2003 to correct PN field.)
 CX
 CX Sequence 9 AA;
 CX
 CX Query Match 100.0%; Score 45; DB 15; Length 9;
 CX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 CX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CX
 CX QY 1 VLHKRTLGL 9
 CX . |||||
 CX DB 1 VLHKRTLGL 9
 CX
 CX RESULT 2
 CX AAM52980
 CX ID AAM52980 standard; peptide; 9 AA.
 CX CX
 CX AAM52980;
 CX 12-MAR-2002 (first entry)
 CX Hepatitis B virus X protein peptide (residues 92-100).
 CX
 CX HBV; X protein; cytotoxic T-lymphocyte; CTL; MHC class I;
 CX major histocompatibility complex; immunomodulator.
 CX
 CX Hepatitis B virus.
 CX
 CX KR98022440-A.
 CX PD 06-JUL-1998.
 CX PF 23-SEP-1996; 96KR-0041612.
 CX PR 23-SEP-1996; 96KR-0041612.
 CX PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
 CX PI Park SH, Chung MG, Lee HG, Yoon HS, Min SS, Lee TG, Lim JS;
 CX WPI; 1999-300977/25.
 CX Synthetic peptide having immunoregulating activities for hepatitis B
 CX virus -
 CX
 CX Example 1; Page 4; 7pp; Korean.
 CX
 CX The invention relates to peptides derived from the hepatitis B virus
 CX (HBV) X protein (AAM52970-AAM52973). The peptides are presented on major
 CX histocompatibility complex (MHC) class I molecules and act as cytotoxic
 CX T-lymphocyte (CTL) epitopes. Sequences AAM52974-AAM52984 represent HBV
 CX X protein-derived peptides used in an exemplification of the invention.
 CX
 CX Sequence 9 AA;
 CX
 CX Query Match 100.0%; Score 45; DB 20; Length 9;
 CX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 CX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CX
 CX QY 1 VLHKRTLGL 9
 CX . |||||
 CX DB 1 VLHKRTLGL 9
 CX
 CX RESULT 4
 CX ABJ06345
 CX ID ABJ06345 standard; Peptide; 9 AA.
 CX XX
 CX AC ABJ06345;
 CX XX

CX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 CX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CX
 CX QY 1 VLHKRTLGL 9
 CX . |||||
 CX DB 1 VLHKRTLGL 9
 CX
 CX RESULT 3
 CX AAY24460
 CX ID AAY24460 standard; peptide; 9 AA.
 CX XX
 CX AAY24460;
 CX 23-SEP-1999 (first entry)
 CX Hepatitis B virus X protein peptide #2.
 CX
 CX Hepatitis B virus; HBV; X protein; cytotoxic T lymphocyte; liposome;
 CX CTL; antigen; immunity; liver cancer.
 CX
 CX Hepatitis B virus.
 CX Synthetic.
 CX
 CX W09936434-A1.
 CX PD 22-JUL-1999.
 CX PF 19-JAN-1998; 98WO-KR00010.
 CX PR 19-JAN-1998; 98WO-KR00010.
 CX PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
 CX PI Chang J, Cheong H, Cho S, Choi M, Hwang Y, Kim T;
 CX Lee K;
 CX WPI; 1999-444387/37.
 CX
 CX Hepatitis B virus protein X-derived peptide antigens used to
 CX stimulate cytotoxic T lymphocytes, useful for treatment of
 CX HBV-associated diseases, especially liver cancer
 CX
 CX Claim 2; Page 24; 33pp; English.
 CX
 CX The present invention describes peptide antigens AAY24459 to AAY24463
 CX derived from the X protein of hepatitis B virus (HBV) which are
 CX recognized by cytotoxic T lymphocytes (CTL). The peptide antigens
 CX derived from HBV X protein are useful for inducing CTLs against the
 CX virus or inducing immunological tolerance to the virus. pH-sensitive
 CX liposomes containing the peptide antigens are used to induce cellular
 CX immunity so that CTLs specific to the virus can be produced. This is
 CX useful for prevention and treatment of HBV-associated diseases, permit
 CX especially HBV-associated liver cancer. pH-sensitive liposomes permit
 CX the selective transportation of anti-cancer drugs.
 CX
 CX Sequence 9 AA;
 CX
 CX Query Match 100.0%; Score 45; DB 20; Length 9;
 CX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 CX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CX
 CX QY 1 VLHKRTLGL 9
 CX . |||||
 CX DB 1 VLHKRTLGL 9
 CX
 CX RESULT 4
 CX ABJ06345
 CX ID ABJ06345 standard; Peptide; 9 AA.
 CX XX
 CX AC ABJ06345;
 CX XX

14-NOV-2002 (first entry)
 Hepatitis B virus epitope #563.
 Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 virucide; hepatotropic; antiinflammatory.

Hepatitis B virus.

WO200219986-A1.

14-MAR-2002.

08-SEP-2000; 2000WO-US24802.

08-SEP-2000; 2000WO-US24802.

(EPIM-) EPIMMUNE INC.

(SETT/) SETTE A.

Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 Celis E, Kubo RT, Grey HM, Chesnut RW;

WPI; 2002-643192/69.

Vaccine composition for treating or preventing hepatitis B virus (HBV)
 infection, and/or for stimulating an immune response to HBV, comprises
 a HBV peptide epitope -

Disclosure; Page 122; 228pp; English.

The present invention relates to a composition comprising at least one
 hepatitis B virus epitope. This can be used in the production of a
 vaccine for use in preventing or treating hepatitis B virus infection.
 The present sequence is a peptide described in the exemplification of the
 invention.

Sequence 9 AA;

Query Match 100.0%; Score 45; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. NO. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VLHKRTLGL 9

|||||||

1 VLHKRTLGL 9

SULT 5
 J06875
 ABJ06875 standard; Peptide; 9 AA.

ABJ06875;

14-NOV-2002 (first entry)

Hepatitis B virus epitope #1093.

Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 virucide; hepatotropic; antiinflammatory.

Hepatitis B virus.

WO200219986-A1.

14-MAR-2002.

08-SEP-2000; 2000WO-US24802.

08-SEP-2000; 2000WO-US24802.

(EPIM-) EPIMMUNE INC.

(SETT/) SETTE A.

XX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 PI Celis E, Kubo RT, Grey HM, Chesnut RW;
 XX WPI; 2002-643192/69.
 DR Vaccine composition for treating or preventing hepatitis B virus (HBV)
 PT infection, and/or for stimulating an immune response to HBV, comprises
 PT a HBV peptide epitope -
 XX Disclosure; Page 131; 228pp; English.
 PS
 XX The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention.
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 45; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. NO. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VLHKRTLGL 9

|||||||

1 VLHKRTLGL 9

RESULT 6

ABJ07613

ID ABJ07613 standard; Peptide; 9 AA.

XX AC ABJ07613;

XX DT 14-NOV-2002 (first entry)

XX DE Hepatitis B virus epitope #1831.

XX KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 virucide; hepatotropic; antiinflammatory.

XX OS Hepatitis B virus.

XX PN WO200219986-A1.

XX PD 14-MAR-2002.

XX PF 08-SEP-2000; 2000WO-US24802.

XX PR 08-SEP-2000; 2000WO-US24802.

XX PA (EPIM-) EPIMMUNE INC.

XX PA (SETT/) SETTE A.

XX PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 Celis E, Kubo RT, Grey HM, Chesnut RW;

XX WPI; 2002-643192/69.

XX Vaccine composition for treating or preventing hepatitis B virus (HBV)
 PT infection, and/or for stimulating an immune response to HBV, comprises
 PT a HBV peptide epitope -
 XX Disclosure; Page 147; 228pp; English.

PS

XX The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention.
 XX Sequence 9 AA;

Query Match 100.0%; Score 45; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 VLHKRTLGL 9
 |||||
 2b 1 VLHKRTLGL 9

RESULT 7
 ABJ0841
 ID ABJ0841 standard; Peptide; 9 AA.
 AC ABJ0841;
 DT 14-NOV-2002 (first entry)
 DE Hepatitis B virus epitope #3059.
 EW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 EX virucide; hepatotropic; antiinflammatory.
 FS Hepatitis B virus.
 GN WO200219986-A1.
 HP 14-MAR-2002.
 IP 08-SEP-2000; 2000WO-US24802.
 JQ 08-SEP-2000; 2000WO-US24802.
 KA (EPIM-) EPIMMUNE INC.
 LB (SETT/) SETTE A.
 MC Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 NI Celis E, Kubo RT, Grey HM, Chesnut RW;
 OJ WPI; 2002-643192/69.
 PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
 infection, and/or for stimulating an immune response to HBV, comprises
 a HBV peptide epitope -
 QS Disclosure; Page 178; 228pp; English.
 The present invention relates to a composition comprising at least one
 hepatitis B virus epitope. This can be used in the production of a
 vaccine for use in preventing or treating hepatitis B virus infection.
 The present sequence is a peptide described in the exemplification of the
 invention.

Sequence 9 AA;
 Query Match 100.0%; Score 45; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 VLHKRTLGL 9
 |||||
 b 1 VLHKRTLGL 9

RESULT 8
 BU09133
 ID ABJ09133 standard; Peptide; 9 AA.
 AC ABJ09133;
 DT 14-NOV-2002 (first entry)
 DE Hepatitis B virus epitope #3351.

XX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 KW virucide; hepatotropic; antiinflammatory.
 OS Hepatitis B virus.
 XX WO200219986-A1.
 XX PD 14-MAR-2002.
 XX PF 08-SEP-2000; 2000WO-US24802.
 XX PR 08-SEP-2000; 2000WO-US24802.
 XX FA (EPIM-) EPIMMUNE INC.
 XX FA (SETT/) SETTE A.
 PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 PI Celis E, Kubo RT, Grey HM, Chesnut RW;
 XX WPI; 2002-643192/69.
 DR Vaccine composition for treating or preventing hepatitis B virus (HBV)
 infection, and/or for stimulating an immune response to HBV, comprises
 a HBV peptide epitope -
 XX Disclosure; Page 181; 228pp; English.
 XX The present invention relates to a composition comprising at least one
 hepatitis B virus epitope. This can be used in the production of a
 vaccine for use in preventing or treating hepatitis B virus infection.
 The present sequence is a peptide described in the exemplification of the
 invention.

Sequence 9 AA;
 Query Match 100.0%; Score 45; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
 |||||
 Db 1 VLHKRTLGL 9

RESULT 9
 AAMS2970
 ID AAMS2970 standard; peptide; 10 AA.
 AC AAMS2970;
 DT 12-MAR-2002 (first entry)
 DE Hepatitis B virus X protein CTL epitope (residues 91-100), SEQ ID NO:1.
 EW HBV; X protein; cytotoxic T-lymphocyte; CTL; MHC class I; epitope;
 KW major histocompatibility complex; immunomodulator.
 XX Hepatitis B virus.
 XX KR98022440-A.
 XX PD 06-JUL-1998.
 XX PF 23-SEP-1996; 96KR-0041612.
 XX PR 23-SEP-1996; 96KR-0041612.
 XX PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
 XX PI Park SH, Chung MG, Lee HG, Yoon HS, Min SS, Lee TG, Lim JS;
 XX WPI; 1999-300977/25.

Synthetic peptide having immunoregulating activities for hepatitis B virus -

Claim 3; Page 4; 7pp; Korean.

The invention relates to peptides derived from the hepatitis B virus (HBV) X protein (AAM52970-AAM52973). The peptides are presented on major histocompatibility complex (MHC) class I molecules and act as cytotoxic T-lymphocyte (CTL) epitopes. The present sequence represents a specifically claimed HBV X protein CTL epitope of the invention.

Sequence 10 AA;

Query Match 100.0%; Score 45; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VLHKRTLGL 9
|||||||
2 VLHKRTLGL 10

ULT 10
06135

ABJ06135 standard; Peptide; 10 AA.

ABJ06135;

14-NOV-2002 (first entry)

Hepatitis B virus epitope #353.

Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis; virucide; hepatotropic; antiinflammatory.

Hepatitis B virus.

WO200219986-A1.

14-MAR-2002.

08-SEP-2000; 2000WO-US24802.

08-SEP-2000; 2000WO-US24802.

(EPIM-) EPIMMUNE INC.

(SETT/) SETTE A.

Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD; Celis E, Kubo RT, Grey HM, Chesnut RW;

WPI; 2002-643192/69.

Vaccine composition for treating or preventing hepatitis B virus (HBV) infection, and/or for stimulating an immune response to HBV, comprises a HBV peptide epitope -

Disclosure; Page 117; 228pp; English.

The present invention relates to a composition comprising at least one hepatitis B virus epitope. This can be used in the production of a vaccine for use in preventing or treating hepatitis B virus infection. The present sequence is a peptide described in the exemplification of the invention.

Sequence 10 AA;

Query Match 100.0%; Score 45; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VLHKRTLGL 9

Db 2 VLHKRTLGL 10
|||||||

RESULT 11

ABJ06665
ID ABJ06665 standard; Peptide; 10 AA.

XX AC ABJ06665;

XX DT 14-NOV-2002 (first entry)

XX DE Hepatitis B virus epitope #883.

XX KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis; virucide; hepatotropic; antiinflammatory.

XX OS Hepatitis B virus.

XX PN WO200219986-A1.

XX PD 14-MAR-2002.

XX PF 08-SEP-2000; 2000WO-US24802.

XX PR 08-SEP-2000; 2000WO-US24802.

XX PA (EPIM-) EPIMMUNE INC.

XX PA (SETT/) SETTE A.

XX PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD; Celis E, Kubo RT, Grey HM, Chesnut RW;

XX DR WPI; 2002-643192/69.

XX PT Vaccine composition for treating or preventing hepatitis B virus (HBV) infection, and/or for stimulating an immune response to HBV, comprises a HBV peptide epitope -

XX PS Disclosure; Page 128; 228pp; English.

XX CC The present invention relates to a composition comprising at least one hepatitis B virus epitope. This can be used in the production of a vaccine for use in preventing or treating hepatitis B virus infection. The present sequence is a peptide described in the exemplification of the invention.

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 45; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLHKRTLGL 9

Db 2 VLHKRTLGL 10
|||||||

RESULT 12

ABJ07674
ID ABJ07674 standard; Peptide; 10 AA.

XX AC ABJ07674;

XX DT 14-NOV-2002 (first entry)

XX DE Hepatitis B virus epitope #1892.

XX KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis; virucide; hepatotropic; antiinflammatory.

XX OS Hepatitis B virus.

LT 15
9280
ABJ09280 standard; Peptide; 15 AA.

ABJ09280;

14-NOV-2002 (first entry)

Hepatitis B virus epitope #3498.

Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis; virucide; hepatotropic; antiinflammatory.

Hepatitis B virus.

WO200219986-A1.

14-MAR-2002.

08-SEP-2000; 2000WO-US24802.

08-SEP-2000; 2000WO-US24802.

(EPIM-) EPIMMUNE INC.
(SETT) SETTE A.

Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
Celis E, Kubo RT, Grey HM, Chesnut RW,

WPI; 2002-643192/69.

Vaccine composition for treating or preventing hepatitis B virus (HBV) infection, and/or for stimulating an immune response to HBV, comprises a HBV peptide epitope -

Disclosure; Page 182; 228pp; English.

The present invention relates to a composition comprising at least one hepatitis B virus epitope. This can be used in the production of a vaccine for use in preventing or treating hepatitis B virus infection. The present sequence is a peptide described in the exemplification of the invention.

Sequence 15 AA;

Very Match 100.0%; Score 45; DB 23; Length 15;
Fast Local Similarity 100.0%; Pred. No. 0.0079;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VLHKRTLGL 9
|||||
4 VLHKRTLGL 12

Job completed: December 23, 2003, 08:44:00
Time: 26.8 secs